



# Sequence Listing

<110> de Sauvage, Frederic  
Carpenter, David A.

<120> Patched-2 Antibodies

<130> P1405R1C1

<140> US 09/293,505

<141> 1999-04-14

<150> US 60/081,884

<151> 1998-04-15

<160> 24

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<211> 4030

<212> DNA

<213> Homo sapiens

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BEST AVAILABLE COPY

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<211> 1203

<212> PRT

<213> Homo sapiens

<400> 2

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Lys	Ala	Pro	Leu	Trp	Leu	Arg	Ala	Tyr	Phe	Gln	Gly	Leu	Leu	Phe	
				35					40					45	
Ser	Leu	Gly	Cys	Gly	Ile	Gln	Arg	His	Cys	Gly	Lys	Val	Leu	Phe	
				50					55					60	
Leu	Gly	Leu	Leu	Ala	Phe	Gly	Ala	Leu	Ala	Leu	Gly	Leu	Arg	Met	
				65					70					75	
Ala	Ile	Ile	Glu	Thr	Asn	Leu	Glu	Gln	Leu	Trp	Val	Glu	Val	Gly	
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Ser	Arg	Val	Ser	Gln	Glu	Leu	His	Tyr	Thr	Lys	Glu	Lys	Leu	Gly	
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Glu	Glu	Ala	Ala	Tyr	Thr	Ser	Gln	Met	Leu	Ile	Gln	Thr	Ala	Arg	
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Gln	Glu	Gly	Glu	Asn	Ile	Leu	Thr	Pro	Glu	Ala	Leu	Gly	Leu	His	
				125					130					135	
Leu	Gln	Ala	Ala	Leu	Thr	Ala	Ser	Lys	Val	Gln	Val	Ser	Leu	Tyr	
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Gly	Lys	Ser	Trp	Asp	Leu	Asn	Lys	Ile	Cys	Tyr	Lys	Ser	Gly	Val	
				155					160					165	
Pro	Leu	Ile	Glu	Asn	Gly	Met	Ile	Glu	Trp	Met	Ile	Glu	Lys	Leu	
				170					175					180	
Phe	Pro	Cys	Val	Ile	Leu	Thr	Pro	Leu	Asp	Cys	Phe	Trp	Glu	Gly	
				185					190					195	
Ala	Lys	Leu	Gln	Gly	Gly	Ser	Ala	Tyr	Leu	Pro	Gly	Arg	Pro	Asp	
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Ile	Gln	Trp	Thr	Asn	Leu	Asp	Pro	Glu	Gln	Leu	Leu	Glu	Glu	Leu	
				215					220					225	
Gly	Pro	Phe	Ala	Ser	Leu	Glu	Gly	Phe	Arg	Glu	Leu	Leu	Asp	Lys	
				230					235					240	
Ala	Gln	Val	Gly	Gln	Ala	Tyr	Val	Gly	Arg	Pro	Cys	Leu	His	Pro	
				245					250					255	
Asp	Asp	Leu	His	Cys	Pro	Pro	Ser	Ala	Pro	Asn	His	His	Ser	Arg	
				260					265					270	

Gln Ala Pro Asn Val Ala His Glu Leu Ser Gly Gly Cys His Gly	275	280	285
Phe Ser His Lys Phe Met His Trp Gln Glu Glu Leu Leu Leu Gly	290	295	300
Gly Met Ala Arg Asp Pro Gln Gly Glu Leu Leu Arg Ala Glu Ala	305	310	315
Leu Gln Ser Thr Phe Leu Leu Met Ser Pro Arg Gln Leu Tyr Glu	320	325	330
His Phe Arg Gly Asp Tyr Gln Thr His Asp Ile Gly Trp Ser Glu	335	340	345
Glu Gln Ala Ser Thr Val Leu Gln Ala Trp Gln Arg Arg Phe Val	350	355	360
Gln Leu Ala Gln Glu Ala Leu Pro Glu Asn Ala Ser Gln Gln Ile	365	370	375
His Ala Phe Ser Ser Thr Thr Leu Asp Asp Ile Leu His Ala Phe	380	385	390
Ser Glu Val Ser Ala Ala Arg Val Val Gly Gly Tyr Leu Leu Met	395	400	405
Leu Ala Tyr Ala Cys Val Thr Met Leu Arg Trp Asp Cys Ala Gln	410	415	420
Ser Gln Gly Ser Val Gly Leu Ala Gly Val Leu Leu Val Ala Leu	425	430	435
Ala Val Ala Ser Gly Leu Gly Leu Cys Ala Leu Leu Gly Ile Thr	440	445	450
Phe Asn Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly	455	460	465
Ile Gly Val Asp Asp Val Phe Leu Leu Ala His Ala Phe Thr Glu	470	475	480
Ala Leu Pro Gly Thr Pro Leu Gln Glu Arg Met Gly Glu Cys Leu	485	490	495
Gln Arg Thr Gly Thr Ser Val Val Leu Thr Ser Ile Asn Asn Met	500	505	510
Ala Ala Phe Leu Met Ala Ala Leu Val Pro Ile Pro Ala Leu Arg	515	520	525
Ala Phe Ser Leu Gln Ala Ala Ile Val Val Gly Cys Thr Phe Val	530	535	540
Ala Val Met Leu Val Phe Pro Ala Ile Leu Ser Leu Asp Leu Arg	545	550	555
Arg Arg His Cys Gln Arg Leu Asp Val Leu Cys Cys Phe Ser Ser	560	565	570

Pro Cys Ser Ala Gln Val Ile Gln Ile Leu Pro Gln Glu Leu Gly	575	580	585
Asp Gly Thr Val Pro Val Gly Ile Ala His Leu Thr Ala Thr Val	590	595	600
Gln Ala Phe Thr His Cys Glu Ala Ser Ser Gln His Val Val Thr	605	610	615
Ile Leu Pro Pro Gln Ala His Leu Val Pro Pro Pro Ser Asp Pro	620	625	630
Leu Gly Ser Glu Leu Phe Ser Pro Gly Gly Ser Thr Arg Asp Leu	635	640	645
Leu Gly Gln Glu Glu Glu Thr Arg Gln Lys Ala Ala Cys Lys Ser	650	655	660
Leu Pro Cys Ala Arg Trp Asn Leu Ala His Phe Ala Arg Tyr Gln	665	670	675
Phe Ala Pro Leu Leu Leu Gln Ser His Ala Lys Ala Ile Val Leu	680	685	690
Val Leu Phe Gly Ala Leu Leu Gly Leu Ser Leu Tyr Gly Ala Thr	695	700	705
Leu Val Gln Asp Gly Leu Ala Leu Thr Asp Val Val Pro Arg Gly	710	715	720
Thr Lys Glu His Ala Phe Leu Ser Ala Gln Leu Arg Tyr Phe Ser	725	730	735
Leu Tyr Glu Val Ala Leu Val Thr Gln Gly Gly Phe Asp Tyr Ala	740	745	750
His Ser Gln Arg Ala Leu Phe Asp Leu His Gln Arg Phe Ser Ser	755	760	765
Leu Lys Ala Val Leu Pro Pro Pro Ala Thr Gln Ala Pro Arg Thr	770	775	780
Trp Leu His Tyr Tyr Arg Asn Trp Leu Gln Gly Ile Gln Ala Ala	785	790	795
Phe Asp Gln Asp Trp Ala Ser Gly Arg Ile Thr Arg His Ser Tyr	800	805	810
Arg Asn Gly Ser Glu Asp Gly Ala Leu Ala Tyr Lys Leu Leu Ile	815	820	825
Gln Thr Gly Asp Ala Gln Glu Pro Leu Asp Phe Ser Gln Leu Thr	830	835	840
Thr Arg Lys Leu Val Asp Arg Glu Gly Leu Ile Pro Pro Glu Leu	845	850	855
Phe Tyr Met Gly Leu Thr Val Trp Val Ser Ser Asp Pro Leu Gly	860	865	870
Leu Ala Ala Ser Gln Ala Asn Phe Tyr Pro Pro Pro Pro Glu Trp			

875	880	885
Leu His Asp Lys Tyr Asp Thr Thr Gly Glu Asn Leu Arg Ile Pro	890	895 900
Pro Ala Gln Pro Leu Glu Phe Ala Gln Phe Pro Phe Leu Leu Arg	905	910 915
Gly Leu Gln Lys Thr Ala Asp Phe Val Glu Ala Ile Glu Gly Ala	920	925 930
Arg Ala Ala Cys Ala Glu Ala Gly Gln Ala Gly Val His Ala Tyr	935	940 945
Pro Ser Gly Ser Pro Phe Leu Phe Trp Glu Gln Tyr Leu Gly Leu	950	955 960
Arg Arg Cys Phe Leu Leu Ala Val Cys Ile Leu Leu Val Cys Thr	965	970 975
Phe Leu Val Cys Ala Leu Leu Leu Leu Asn Pro Trp Thr Ala Gly	980	985 990
Leu Ile Val Leu Val Leu Ala Met Met Thr Val Glu Leu Phe Gly	995	1000 1005
Ile Met Gly Phe Leu Gly Ile Lys Leu Ser Ala Ile Pro Val Val	1010	1015 1020
Ile Leu Val Ala Ser Val Gly Ile Gly Val Glu Phe Thr Val His	1025	1030 1035
Val Ala Leu Gly Phe Leu Thr Thr Gln Gly Ser Arg Asn Leu Arg	1040	1045 1050
Ala Ala His Ala Leu Glu His Thr Phe Ala Pro Val Thr Asp Gly	1055	1060 1065
Ala Ile Ser Thr Leu Leu Gly Leu Leu Met Leu Ala Gly Ser His	1070	1075 1080
Phe Asp Phe Ile Val Arg Tyr Phe Phe Ala Ala Leu Thr Val Leu	1085	1090 1095
Thr Leu Leu Gly Leu Leu His Gly Leu Val Leu Leu Pro Val Leu	1100	1105 1110
Leu Ser Ile Leu Gly Pro Pro Pro Glu Val Ile Gln Met Tyr Lys	1115	1120 1125
Glu Ser Pro Glu Ile Leu Ser Pro Pro Ala Pro Gln Gly Gly Gly	1130	1135 1140
Leu Arg Trp Gly Ala Ser Ser Ser Leu Pro Gln Ser Phe Ala Arg	1145	1150 1155
Val Thr Thr Ser Met Thr Val Ala Ile His Pro Pro Pro Leu Pro	1160	1165 1170
Gly Ala Tyr Ile His Pro Ala Pro Asp Glu Pro Pro Trp Ser Pro	1175	1180 1185

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Ala Thr Gly

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<211> 228  
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gatgggcctc atcggaatca agctcagt 228

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<213> Homo sapiens

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35 40 45  
Asp Arg Asp Tyr Leu His Arg Pro Ser Tyr Cys Asp Ala Ala Phe  
50 55 60  
Ala Leu Glu Gln Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala  
65 70 75  
Pro Leu Trp Leu Arg Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu  
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Gly Cys Tyr Ile Gln Lys Asn Cys Gly Lys Ala Met Phe Asn Pro  
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Gln Leu Met Ile Gln Thr Pro Lys Glu Glu Gly Ala Asn Val Leu  
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Ser Arg Val His Val Tyr Met Tyr Asn Arg Gln Trp Lys Leu Glu  
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His Leu Cys Tyr Lys Ser Gly Glu Leu Ile Thr Glu Thr Gly Tyr  
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Met Asp Gln Ile Ile Glu Tyr Leu Tyr Pro Cys Leu Ile Ile Thr  
170 175 180  
Pro Leu Asp Cys Phe Trp Glu Gly Ala Lys Leu Gln Ser Gly Thr  
185 190 195  
Ala Tyr Leu Leu Gly Lys Pro Pro Leu Arg Trp Thr Asn Phe Asp

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Pro Leu Glu Phe	Leu Glu Glu Leu Lys	Lys Ile Asn Tyr Gln	Val
	215	220	225
Asp Ser Trp Glu	Glu Met Leu Asn Lys	Ala Glu Val Gly His	Gly
	230	235	240
Tyr Met Asp Arg	Pro Cys Leu Asn Pro	Ala Asp Pro Asp Cys	Pro
	245	250	255
Ala Thr Ala Pro	Asn Lys Asn Ser Thr	Lys Pro Leu Asp Met	Ala
	260	265	270
Leu Val Leu Asn	Gly Gly Cys His Gly	Leu Ser Arg Lys Tyr	Met
	275	280	285
His Trp Gln Glu	Glu Leu Ile Val Gly	Gly Thr Val Lys Asn	Ser
	290	295	300
Thr Gly Lys Leu	Val Ser Ala His Ala	Leu Gln Thr Met Phe	Gln
	305	310	315
Leu Met Thr Pro	Lys Gln Met Tyr Glu	His Phe Lys Gly Tyr	Glu
	320	325	330
Tyr Val Ser His	Ile Asn Trp Asn Glu	Asp Lys Ala Ala Ala	Ile
	335	340	345
Leu Glu Ala Trp	Gln Arg Thr Tyr Val	Glu Val Val His Gln	Ser
	350	355	360
Val Ala Gln Asn	Ser Thr Gln Lys Val	Leu Ser Phe Thr Thr	Thr
	365	370	375
Thr Leu Asp Asp	Ile Leu Lys Ser Phe	Ser Asp Val Ser Val	Ile
	380	385	390
Arg Val Ala Ser	Gly Tyr Leu Leu Met	Leu Ala Tyr Ala Cys	Leu
	395	400	405
Thr Met Leu Arg	Trp Asp Cys Ser Lys	Ser Gln Gly Ala Val	Gly
	410	415	420
Leu Ala Gly Val	Leu Leu Val Ala Leu	Ser Val Ala Ala Gly	Leu
	425	430	435
Gly Leu Cys Ser	Leu Ile Gly Ile Ser	Phe Asn Ala Ala Thr	Thr
	440	445	450
Gln Val Leu Pro	Phe Leu Ala Leu Gly	Val Gly Val Asp Asp	Val
	455	460	465
Phe Leu Leu Ala	His Ala Phe Ser Glu	Thr Gly Gln Asn Lys	Arg
	470	475	480
Ile Pro Phe Glu	Asp Arg Thr Gly Glu	Cys Leu Lys Arg Thr	Gly
	485	490	495
Ala Ser Val Ala	Leu Thr Ser Ile Ser	Asn Val Thr Ala Phe	Phe
	500	505	510

Met	Ala	Ala	Leu	Ile	Pro	Ile	Pro	Ala	Leu	Arg	Ala	Phe	Ser	Leu		515	520	525
Gln	Ala	Ala	Val	Val	Val	Val	Phe	Asn	Phe	Ala	Met	Val	Leu	Leu		530	535	540
Ile	Phe	Pro	Ala	Ile	Leu	Ser	Met	Asp	Leu	Tyr	Arg	Arg	Glu	Asp		545	550	555
Arg	Arg	Leu	Asp	Ile	Phe	Cys	Cys	Phe	Thr	Ser	Pro	Cys	Val	Ser		560	565	570
Arg	Val	Ile	Gln	Val	Glu	Pro	Gln	Ala	Tyr	Thr	Asp	Thr	His	Asp		575	580	585
Asn	Thr	Arg	Tyr	Ser	Pro	Pro	Pro	Pro	Tyr	Ser	Ser	His	Ser	Phe		590	595	600
Ala	His	Glu	Thr	Gln	Ile	Thr	Met	Gln	Ser	Thr	Val	Gln	Leu	Arg		605	610	615
Thr	Glu	Tyr	Asp	Pro	His	Thr	His	Val	Tyr	Tyr	Thr	Thr	Ala	Glu		620	625	630
Pro	Arg	Ser	Glu	Ile	Ser	Val	Gln	Pro	Val	Thr	Val	Thr	Gln	Asp		635	640	645
Thr	Leu	Ser	Cys	Gln	Ser	Pro	Glu	Ser	Thr	Ser	Ser	Thr	Arg	Asp		650	655	660
Leu	Leu	Ser	Gln	Phe	Ser	Asp	Ser	Ser	Leu	His	Cys	Leu	Glu	Pro		665	670	675
Pro	Cys	Thr	Lys	Trp	Thr	Leu	Ser	Ser	Phe	Ala	Glu	Lys	His	Tyr		680	685	690
Ala	Pro	Phe	Leu	Leu	Lys	Pro	Lys	Ala	Lys	Val	Val	Val	Ile	Phe		695	700	705
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Val	Arg	Asp	Gly	Leu	Asp	Leu	Thr	Asp	Ile	Val	Pro	Arg	Glu	Thr		725	730	735
Arg	Glu	Tyr	Asp	Phe	Ile	Ala	Ala	Gln	Phe	Lys	Tyr	Phe	Ser	Phe		740	745	750
Tyr	Asn	Met	Tyr	Ile	Val	Thr	Gln	Lys	Ala	Asp	Tyr	Pro	Asn	Ile		755	760	765
Gln	His	Leu	Leu	Tyr	Asp	Leu	His	Arg	Ser	Phe	Ser	Asn	Val	Lys		770	775	780
Tyr	Val	Met	Leu	Glu	Glu	Asn	Lys	Gln	Leu	Pro	Lys	Met	Trp	Leu		785	790	795
His	Tyr	Phe	Arg	Asp	Trp	Leu	Gln	Gly	Leu	Gln	Asp	Ala	Phe	Asp		800	805	810

Ser Asp Trp Glu Thr Gly Lys Ile Met Pro Asn Asn Tyr Lys Asn	815	820	825
Gly Ser Asp Asp Gly Val Leu Ala Tyr Lys Leu Leu Val Gln Thr	830	835	840
Gly Ser Arg Asp Lys Pro Ile Asp Ile Ser Gln Leu Thr Lys Gln	845	850	855
Arg Leu Val Asp Ala Asp Gly Ile Ile Asn Pro Ser Ala Phe Tyr	860	865	870
Ile Tyr Leu Thr Ala Trp Val Ser Asn Asp Pro Val Ala Tyr Ala	875	880	885
Ala Ser Gln Ala Asn Ile Arg Pro His Arg Pro Glu Trp Val His	890	895	900
Asp Lys Ala Asp Tyr Met Pro Glu Thr Arg Leu Arg Ile Pro Ala	905	910	915
Ala Glu Pro Ile Glu Tyr Ala Gln Phe Pro Phe Tyr Leu Asn Gly	920	925	930
Leu Arg Asp Thr Ser Asp Phe Val Glu Ala Ile Glu Lys Val Arg	935	940	945
Thr Ile Cys Ser Asn Tyr Thr Ser Leu Gly Leu Ser Ser Tyr Pro	950	955	960
Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile Gly Leu Arg	965	970	975
His Trp Leu Leu Leu Phe Ile Ser Val Val Leu Ala Cys Thr Phe	980	985	990
Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly Ile	995	1000	1005
Ile Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met	1010	1015	1020
Met Gly Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile	1025	1030	1035
Leu Ile Ala Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val	1040	1045	1050
Ala Leu Ala Phe Leu Thr Ala Ile Gly Asp Lys Asn Arg Arg Ala	1055	1060	1065
Val Leu Ala Leu Glu His Met Phe Ala Pro Val Leu Asp Gly Ala	1070	1075	1080
Val Ser Thr Leu Leu Gly Val Leu Met Leu Ala Gly Ser Glu Phe	1085	1090	1095
Asp Phe Ile Val Arg Tyr Phe Phe Ala Val Leu Ala Ile Leu Thr	1100	1105	1110
Ile Leu Gly Val Leu Asn Gly Leu Val Leu Leu Pro Val Leu Leu			

1115	1120	1125
Ser Phe Phe Gly Pro Tyr Pro Glu Val Ser Pro Ala Asn Gly Leu		
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Asn Arg Leu Pro Thr Pro Ser Pro Glu Pro Pro Pro Ser Val Val		
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Arg Phe Ala Met Pro Pro Gly His Thr His Ser Gly Ser Asp Ser		
1160	1165	1170
Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr Val Ser Gly Leu Ser		
1175	1180	1185
Glu Glu Leu Arg His Tyr Glu Ala Gln Gln Gly Ala Gly Gly Pro		
1190	1195	1200
Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro Val Phe Ala		
1205	1210	1215
His Ser Thr Val Val His Pro Glu Ser Arg His His Pro Pro Ser		
1220	1225	1230
Asn Pro Arg Gln Gln Pro His Leu Asp Ser Gly Ser Leu Pro Pro		
1235	1240	1245
Gly Arg Gln Gly Gln Gln Pro Arg Arg Asp Pro Pro Arg Glu Gly		
1250	1255	1260
Leu Trp Pro Pro Leu Tyr Arg Pro Arg Arg Asp Ala Phe Glu Ile		
1265	1270	1275
Ser Thr Glu Gly His Ser Gly Pro Ser Asn Arg Ala Arg Trp Gly		
1280	1285	1290
Pro Arg Gly Ala Arg Ser His Asn Pro Arg Asn Pro Ala Ser Thr		
1295	1300	1305
Ala Met Gly Ser Ser Val Pro Gly Tyr Cys Gln Pro Ile Thr Thr		
1310	1315	1320
Val Thr Ala Ser Ala Ser Val Thr Val Ala Val His Pro Pro Pro		
1325	1330	1335
Val Pro Gly Pro Gly Arg Asn Pro Arg Gly Gly Leu Cys Pro Gly		
1340	1345	1350
Tyr Pro Glu Thr Asp His Gly Leu Phe Glu Asp Pro His Val Pro		
1355	1360	1365
Phe His Val Arg Cys Glu Arg Arg Asp Ser Lys Val Glu Val Ile		
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Glu Leu Gln Asp Val Glu Cys Glu Glu Arg Pro Arg Gly Ser Ser		
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Ser Asn		

<210> 8

<211> 1182

<212> PRT

<213> Mus musculus

<400> 8

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				20					25					30
Gln	Ala	Pro	Leu	Trp	Leu	Arg	Ala	Tyr	Phe	Gln	Gly	Leu	Leu	Phe
				35					40					45
Ser	Leu	Gly	Cys	Arg	Ile	Gln	Lys	His	Cys	Gly	Lys	Val	Leu	Phe
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Leu	Gly	Leu	Val	Ala	Phe	Gly	Ala	Leu	Ala	Leu	Gly	Leu	Arg	Val
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Ala	Val	Ile	Glu	Thr	Asp	Leu	Glu	Gln	Leu	Trp	Val	Glu	Val	Gly
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Ser	Arg	Val	Ser	Gln	Glu	Leu	His	Tyr	Thr	Lys	Glu	Lys	Leu	Gly
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Glu	Glu	Ala	Ala	Tyr	Thr	Ser	Gln	Met	Leu	Ile	Gln	Thr	Ala	His
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Gln	Glu	Gly	Gly	Asn	Val	Leu	Thr	Pro	Glu	Ala	Leu	Asp	Leu	His
				125					130					135
Leu	Gln	Ala	Ala	Leu	Thr	Ala	Ser	Lys	Val	Gln	Val	Ser	Leu	Tyr
				140					145					150
Gly	Lys	Ser	Trp	Asp	Leu	Asn	Lys	Ile	Cys	Tyr	Lys	Ser	Gly	Val
				155					160					165
Pro	Leu	Ile	Glu	Asn	Gly	Met	Ile	Glu	Arg	Met	Ile	Glu	Lys	Leu
				170					175					180
Phe	Pro	Cys	Val	Ile	Leu	Thr	Pro	Leu	Asp	Cys	Phe	Trp	Glu	Gly
				185					190					195
Ala	Lys	Leu	Gln	Gly	Gly	Ser	Ala	Tyr	Leu	Pro	Gly	Arg	Pro	Asp
				200					205					210
Ile	Gln	Trp	Thr	Asn	Leu	Asp	Pro	Gln	Gln	Leu	Leu	Glu	Glu	Leu
				215					220					225
Gly	Pro	Phe	Ala	Ser	Leu	Glu	Gly	Phe	Arg	Glu	Leu	Leu	Asp	Lys
				230					235					240
Ala	Gln	Val	Gly	Gln	Ala	Tyr	Val	Gly	Arg	Pro	Cys	Leu	Asp	Pro
				245					250					255
Asp	Asp	Pro	His	Cys	Pro	Pro	Ser	Ala	Pro	Asn	Arg	His	Ser	Arg
				260					265					270
Gln	Ala	Pro	Asn	Val	Ala	Gln	Glu	Leu	Ser	Gly	Gly	Cys	His	Gly
				275					280					285

Phe Ser His Lys	Phe Met His Trp Gln	Glu Glu Leu Leu Leu Gly	290	295	300
Gly Thr Ala Arg	Asp Leu Gln Gly Gln	Leu Leu Arg Ala Glu Ala	305	310	315
Leu Gln Ser Thr	Phe Leu Leu Met Ser	Pro Arg Gln Leu Tyr Glu	320	325	330
His Phe Arg Gly	Asp Tyr Gln Thr His	Asp Ile Gly Trp Ser Glu	335	340	345
Glu Gln Ala Ser	Met Val Leu Gln Ala	Trp Gln Arg Arg Phe Val	350	355	360
Gln Leu Ala Gln	Glu Ala Leu Pro Ala	Asn Ala Ser Gln Gln Ile	365	370	375
His Ala Phe Ser	Ser Thr Thr Leu Asp	Asp Ile Leu Arg Ala Phe	380	385	390
Ser Glu Val Ser	Thr Thr Arg Val Val	Gly Gly Tyr Leu Leu Met	395	400	405
Leu Ala Tyr Ala	Cys Val Thr Met Leu	Arg Trp Asp Cys Ala Gln	410	415	420
Ser Gln Gly Ala	Val Gly Leu Ala Gly	Val Leu Leu Val Ala Leu	425	430	435
Ala Val Ala Ser	Gly Leu Gly Leu Cys	Ala Leu Leu Gly Ile Thr	440	445	450
Phe Asn Ala Ala	Thr Thr Gln Val Leu	Pro Phe Leu Ala Leu Gly	455	460	465
Ile Gly Val Asp	Asp Ile Phe Leu Leu	Ala His Ala Phe Thr Lys	470	475	480
Ala Pro Pro Asp	Thr Pro Leu Pro Glu	Arg Met Gly Glu Cys Leu	485	490	495
Arg Ser Thr Gly	Thr Ser Val Ala Leu	Thr Ser Val Asn Asn Met	500	505	510
Val Ala Phe Phe	Met Ala Ala Leu Val	Pro Ile Pro Ala Leu Arg	515	520	525
Ala Phe Ser Leu	Gln Ala Ala Ile Val	Val Gly Cys Asn Phe Ala	530	535	540
Ala Val Met Leu	Val Phe Pro Ala Ile	Leu Ser Leu Asp Leu Arg	545	550	555
Arg Arg His Arg	Gln Arg Leu Asp Val	Leu Cys Cys Phe Ser Ser	560	565	570
Pro Cys Ser Ala	Gln Val Ile Gln Met	Leu Pro Gln Glu Leu Gly	575	580	585
Asp Arg Ala Val	Pro Val Gly Ile Ala	His Leu Thr Ala Thr Val			

590	595	600
Gln Ala Phe Thr His Cys Glu Ala Ser	Ser Gln His Val Val Thr	
605	610	615
Ile Leu Pro Pro Gln Ala His Leu Leu Ser	Pro Ala Ser Asp Pro	
620	625	630
Leu Gly Ser Glu Leu Tyr Ser Pro Gly Gly Ser Thr Arg Asp Leu		
635	640	645
Leu Ser Gln Glu Glu Gly Thr Gly Pro Gln Ala Ala Cys Arg Pro		
650	655	660
Leu Leu Cys Ala His Trp Thr Leu Ala His Phe Ala Arg Tyr Gln		
665	670	675
Phe Ala Pro Leu Leu Leu Gln Thr Arg Ala Lys Ala Leu Val Leu		
680	685	690
Leu Phe Phe Gly Ala Leu Leu Gly Leu Ser Leu Tyr Gly Ala Thr		
695	700	705
Leu Val Gln Asp Gly Leu Ala Leu Thr Asp Val Val Pro Arg Gly		
710	715	720
Thr Lys Glu His Ala Phe Leu Ser Ala Gln Leu Arg Tyr Phe Ser		
725	730	735
Leu Tyr Glu Val Ala Leu Val Thr Gln Gly Gly Phe Asp Tyr Ala		
740	745	750
His Ser Gln Arg Ala Leu Phe Asp Leu His Gln Arg Phe Ser Ser		
755	760	765
Leu Lys Ala Val Leu Pro Pro Pro Ala Thr Gln Ala Pro Arg Thr		
770	775	780
Trp Leu His Tyr Tyr Arg Ser Trp Leu Gln Gly Ile Gln Ala Ala		
785	790	795
Phe Asp Gln Asp Trp Ala Ser Gly Arg Ile Thr Cys His Ser Tyr		
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Arg Asn Gly Ser Glu Asp Gly Ala Leu Ala Tyr Lys Leu Leu Ile		
815	820	825
Gln Thr Gly Asn Ala Gln Glu Pro Leu Asp Phe Ser Gln Leu Thr		
830	835	840
Thr Arg Lys Leu Val Asp Lys Glu Gly Leu Ile Pro Pro Glu Leu		
845	850	855
Phe Tyr Met Gly Leu Thr Val Trp Val Ser Ser Asp Pro Leu Gly		
860	865	870
Leu Ala Ala Ser Gln Ala Asn Phe Tyr Pro Pro Pro Pro Glu Trp		
875	880	885
Leu His Asp Lys Tyr Asp Thr Thr Gly Glu Asn Leu Arg Ile Pro		
890	895	900

Ala Ala Gln Pro Leu Glu Phe Ala Gln Phe Pro Phe Leu Leu His	905	910	915
Gly Leu Gln Lys Thr Ala Asp Phe Val Glu Ala Ile Glu Gly Ala	920	925	930
Arg Ala Ala Cys Thr Glu Ala Gly Gln Ala Gly Val His Ala Tyr	935	940	945
Pro Ser Gly Ser Pro Phe Leu Phe Trp Glu Gln Tyr Leu Gly Leu	950	955	960
Arg Arg Cys Phe Leu Leu Ala Val Cys Ile Leu Leu Val Cys Thr	965	970	975
Phe Leu Val Cys Ala Leu Leu Leu Leu Ser Pro Trp Thr Ala Gly	980	985	990
Leu Ile Val Leu Val Leu Ala Met Met Thr Val Glu Leu Phe Gly	995	1000	1005
Ile Met Gly Phe Leu Gly Ile Lys Leu Ser Ala Ile Pro Val Val	1010	1015	1020
Ile Leu Val Ala Ser Ile Gly Ile Gly Val Glu Phe Thr Val His	1025	1030	1035
Val Ala Leu Gly Phe Leu Thr Ser His Gly Ser Arg Asn Leu Arg	1040	1045	1050
Ala Ala Ser Ala Leu Glu Gln Thr Phe Ala Pro Val Thr Asp Gly	1055	1060	1065
Ala Val Ser Thr Leu Leu Gly Leu Leu Met Leu Ala Gly Ser Asn	1070	1075	1080
Phe Asp Phe Ile Ile Arg Tyr Phe Phe Val Val Leu Thr Val Leu	1085	1090	1095
Thr Leu Leu Gly Leu Leu His Gly Leu Leu Leu Leu Pro Val Leu	1100	1105	1110
Leu Ser Ile Leu Gly Pro Pro Pro Gln Val Val Gln Val Tyr Lys	1115	1120	1125
Glu Ser Pro Gln Thr Leu Asn Ser Ala Ala Pro Gln Arg Gly Gly	1130	1135	1140
Leu Arg Trp Asp Arg Pro Pro Thr Leu Pro Gln Ser Phe Ala Arg	1145	1150	1155
Val Thr Thr Ser Met Thr Val Ala Leu His Pro Pro Pro Leu Pro	1160	1165	1170
Gly Ala Tyr Val His Pro Ala Ser Glu Glu Pro Thr	1175	1180	

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<211> 4004

<212> DNA

<213> Homo sapiens

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<211> 2082

<212> DNA

<213> Homo sapiens

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<212> DNA  
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<210> 15  
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<213> Artificial Sequence  
<220>  
<223> sequence is synthesized  
  
<400> 17  
gcttaggccc gaggagat 18  
  
<210> 18  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> sequence is synthesized  
  
<400> 18  
aactcacaac tttctctcca 20  
  
<210> 19  
<211> 48  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> sequence is synthesized  
  
<400> 19  
ggattctaata acgactcact atagggccca atggcctaaa ccgactgc 48  
  
<210> 20  
<211> 46  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> sequence is synthesized  
  
<400> 20  
ctatgaaatt aaccctcact aaagggaccc acggcctctc ctcaca 46  
  
<210> 21  
<211> 48  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> sequence is synthesized

<400> 21

ggattctaatt acgactcact atagggcccc taaactccgc tgctccac 48

<210> 22

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence is synthesized

<400> 22

ctatgaaatt aaccctcact aaagggagct cccgtgagtc cctatgtg 48

<210> 23

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence is synthesized

<400> 23

tcgacaagca gggaacaccc aagtagaagc tc 32

<210> 24

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence is synthesized

<400> 24

tcgacaagca gggaagtggg aagtagaagc tc 32



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1 GTATTTCAG GCCATGGTGT TCGCGCGAAT TAATCCCGA TCCAGACATG ATAAGATACA TTGATGAGTT TGGACAAACC ACAAATAGAA TGCAGTGA  
 CAATAAAGTC CGGTACCACA ACGCGGCTTA ATTAAGGCT AGGTCTGTAC TATTCTATGT AACTACTCAA ACCTGTTTGG TGTGATCTT ACGTCACTTT

101 AAAATGCTTT ATTGTGAAA TTTGTGATGC TATTGCTTTA TTTGTAACCA TTATAAGCTG CAATAAACAA GTTGGGCCAT GCGGSCAAG CTTCTGCAGG  
 TTTTACGAAA TAAACACTTT AAACACTAGC ATAACGAAAT AAACATTGGT AATATCGAC GTTATTTGTT CAACCCGGTA CCGCCGGTTC GAAGACGTCC

201 TCGACTCTAG AGGATCCCCG GGGAAATCCG GCATGACTCG ATCGCCGCC CACAGAGAGC TGCCCCCGAG TTACACACCC CCAGCTCGAA CCGCAGCACC  
 AGCTGAGATC TCCTAGGGGC CCCTTAAGGC CGTACTGAGC TAGCGGCGGG GAGTCTCTCG ACGGGGCTC AATGTGTGGG GGTGAGCTT GCGTCTGTGG

1 M T R S P P L R E L P P S Y T P P A R T A A P

301 CCAGATCTTA GCTGGGAGCC TGAAGGCTCC ACTCTGGCTT CGTGCTTACT TCCAGGGCCT GCTCTCTCTCT CTGGGATGGG GGATCCAGAG ACATTGTGGC  
 GGTCTAGGAT CGACCCCTCG ACTTCCGAGG TGAGACCGAA GCACGAATGA AGGTCCCGGA CGAGAAGAGA GACCCCTACGC CCTAGGTCTC TGTAACACCG

24 Q I L A G S L K A P L W L R A Y F Q G L L F S L G C G I Q R H C G

401 AAAGTGTCT TTCTGGGACT GTTGGCCTTT GGGGCCCTGG CATTAGTCT CCGCATGGCC ATTATTGAGA CAAACTTGA ACAGCTCTGG GTAGAAGTGG  
 TTTACAGAGA AAGACCTTGA CAACCGGAAA CCCCCGGACC GTAATCCAGA GCGTACCGG TAATAACTCT GTTTGAACCT TGTCGAGACC CATCTTCACC

57 K V L F L G L L A F G A L A L G L R M A I I E T N L E Q L W V E V G

501 GCAGCCGGGT GAGCCAGGAG CTGCATTACA CCAAGGAGAA GCTGGGGGAG GAGGCTGCAT ACACCTCTCA GATGCTGATA CAGACCGCAC GCCAGGAGGG  
 CTGCGGCCCCA CTCGGTCTTC GACGTAATGT GGTTCCTCTT CGACCCCTTC CTCCGACGTA TGTGGAGAGT CTACGACTAT GTCTGGCGTG CCGTCTCTCC

91 S R V S Q E L H Y T K E K L G E E A A Y T S Q M L I Q T A R Q E G

601 AGAGAACATC CTCACACCCG AAGCACTTGG CCTCCACCTC CAGGCAGCCC TCACTGCCAG TAAAGTCCAA GTATCACTCT ATGGGAAGTC CTGGGATTTG  
 TCTCTGTAG GAGTGTGGC TTCGTGAACC GGAGGTGGAG GTCCGTGGG AGTGACGGTC ATTTCAAGTT CAFAGTGAGA TACCCCTCAG GACCCTAAC

124 E N I L T P E A L G L H L Q A A L T A S K V Q V S L Y G K S W D L

701 AACAAAATCT GCTACAAGTC AGGAGTTCCC CTTATTGAAA ATGGATGAT TGAGTGGATG ATTGAGAAGC TGTTCCTGGT CGTGATCCTC ACCCCCCCTCG  
 TTGTTTGA CGATGTTTCA TCCTCAAGG GAATAACTTT TACCTTACTA ACTCACCTAC TAACCTCTCG ACAAGGCAC GCACCTAGGAG TGGGGGAGC

157 N K I C Y K S G V P L I E N G M I E W M I E K L F P C V I L T P L D

FIG. 1A

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801 ACTGCTTCTG GGAGGGAGCC AAACCTCCAAG GGGGCTCCGC CTACCTGCCG GGGCGCCCGG ATATCCAGTG GACCAACCTG GATCCAGAGC AGCTGCTGGA  
TGACGAAGAC CCTCCTCTGG TTGTAGGTTT CCCCAGGCG GATGGACGGG CCGGCGGGCC TATAGTTCAC CTGGTTGGAC CTAGGTCTCG TCGACGACCT  
191 C F W E G A K L Q G G S A Y L P G R P D I Q W T N L D P E Q L L E

901 GGAGCTGGGT CCCTTGCTT CCCTTGAGGG CTTCCTGGGAG CTGCTAGACA AGGCACAGGT GGGCCAGGCC TACGTGGGGC GGCCCTGTCT GCACCCCTGAT  
CCTCGACCCA GGGAACCGA GGGAACCTCC GAAGCCCTC GACGATCTGT TCCGTGTCCA CCCGGTCCGG ATGCACCCCG CCGGGACAGA CGTGGGACTA  
224 E L G P F A S L E G F R E L L D K A Q V G Q A Y V G R P C L H P D

1001 GACCTCCACT GCCCACCTAG TGCCCCCAAC CATCACAGA GGCAGGCTCC CAATGTGGCT CACGAGCTGA GTGGGGGGTG CCATGGCTTC TCCACAAAT  
CTGGAGTGA CCGGTGGATC ACGGGGGTTG GTAGTGTCTG CCGTCCGAGG GTTACACCGA GTGCTCGACT CACCCCGGAC GGTACCGAAG AGGTTGTTTA  
257 D L H C P P S A P N H H S R Q A P N V A H E L S G G C H G F S H K F

1101 TCATGCACTG GCAGGAGGAA TTGCTGCTGG GAGGCATGGC CAGAGACCCC CAGGAGAGC TGCTGAGGC AGAGGCCCTG CAGAGCACCT TCTTGCTGAT  
AGTACGTGAC CGTCCTCCTT AACGAGGACC CTCCGTACCG GTCTCTGGG GTTCTCTCTG ACGACTCCG TCTCCGGGAC GTCTGTTGA AGAAGGACTA  
291 M H W Q E E L L L G G M A R D P Q G E L L R A E A L Q S T F L L M

1201 GAGTCCCCG CAGCTGTACG AGCATTTCCG GGGTGACTAT CAGACACATG ACATTTGGCTG GAGTGAGGAG CAGGCCAGCA CAGTGCTACA AGCCTGGCAG  
CTCAGGGCG GTGACATGC TCGTAAAGG CCCACTGATA GTCTGTGTAC TGTAACCGAC CTCACTCTC GTCCGGTCTG GTCACGATGT TCGGACCGTC  
324 S P R Q L Y E H F R G D Y Q T H D I G W S E E Q A S T V L Q A W Q

1301 CGGCGCTTG TGCAGCTGGC CCAGGAGGCC CTGCCCTGAGA ACGTTTCCA GCAGATCCAT GCCTTCTCCT CCACCACCT GGATGACATC CTGCATGCGT  
GGCGGAAC ACGTCGACCG GGTCTCTCCG GACGGACTCT TCGGAAGGT CGTCTAGGTA CGGAAGAGGA GGTGGTGGGA CCTACTGTAG GACGTACGCA  
357 R R F V Q L A Q E A L P E N A S Q Q I H A F S S T T L D D I L H A F

1401 TCTCTGAAGT CAGTGTGCTCC CGTGTGGTGG GAGGCTATCT GCTCATGCTG GCCTATGCCT GTGTGACCAT GCTGCGGTGG GACTGCGGCC AGTCCCAGGG  
AGAGACTTCA GTACAGACGG GCACACCACC CTCCGATAGA CGAGTAGGAC CGGATACGGA CACACTGGTA CGAGCCACC CTGACGCGGG TCAGGTGCCC  
391 S E V S A A R V V G G Y L L M L A Y A C V T M L R W D C A Q S Q G

1501 TTCCGTGGC CTGCGCGGG TACTGCTGTT GGCCTGGCG GTGGCTCAG GCCTTGGCT CTGTGCCCTG CTGGCATCA CCTTCAATGC TGCCACTACC  
AAGCACCCG GAACGGCCCC ATGACGACCA CCGGACCGC CACCGAGTC CGGAACCGA GACACGGGAC GAGCCGTAGT GGAAGTTACG ACGGTGATGG  
424 S V G L A G V L L V A L A V A S G L G L C A L L G I T F N A A T T

FIG. 1B

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	30	40	50	60	70
905531	GCTGGGGTGCACGCCTACCNCAGCGGNTCCCCCTTCCTCTTCTGGGAACA				
	::: :: : ***** ***** *****				
hpatched	CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCA				
	3010	3020	3030	3040	3050

	80	90	100	110	120
905531	GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGCTCTGCATCCTGCTGG				
	*** * ***** ** * ** * * ***** * * * * *				
hpatched	GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTTCATCAGCGTGGTGTGG				
	3060	3070	3080	3090	3100

	130	140	150	160	170
905531	TGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTNAACCCCTGGACGGCT				
	***** ***** ** * * * * * *****				
hpatched	CCTGCACATTTCCTCGTGTGCGCTGTCTTCCTTCTGAACCCCTGGACGGCC				
	3110	3120	3130	3140	3150

	180	190	200	210	220
905531	GGCCTNATAGTGCTGGTCCTGGCGATGATGACAGTGGAACCTCTTGGTAT				
	** ***** ***** ***** * * * * *				
hpatched	GGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTGTTCCGCAT				
	3160	3170	3180	3190	3200

	230	240	250
905531	CATGGGTTTNCCTGGGCATCAAGCTGAGT		
	***** ** * * * *****		
hpatched	GATGGGCCTCATCGGAATCAAGCTCAGT		
	3210	3220	3230

	80	90	100	110	120
905531	TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGCTCTGCATCCTGCTGGTGT				
	::: ::: * * * * * ***** ***** * * * * *				
hpatched	GCTGCTGCTGTTTCATCAGCGTGGTGTGGCC---TGCACATTTCCTCGTGT				
	3090	3100	3110	3120	

	130	140	150
905531	GCACTTTCCTCGTCTGTGCTCTGCTGCT		
	** * * * * :		
hpatched	GCGCTGTCTTCCTTCTGAACCCCTGGAC		
	3130	3140	3150

FIG. 2A

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```

1326258      30      40      50      60      70
GCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACA
      ::: :: : *****
hpatched     CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCA
      3010      3020      3030      3040      3050

1326258      80      90      100      110      120
GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGG
      *** * ***** ** * *** * ***** * ** * * **
hpatched     GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTTCATCAGCGTGGTGTGG
      3060      3070      3080      3090      3100

1326258      130      140      150
TGTGCACTTTCCTCCTCTGTGCTCT
      *****
hpatched     CCTGCACATTCTCGTGTGCGCTGT
      3110      3120      3130

```

```

1326258      90      100      110      120      130
TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGT
      ::: :: : * * * * * * * * * * * * * * *
hpatched     GCTGCTGCTGTTTCATCAGCGTGGTGTGGCC---TGCACATTCTCGTGT
      3090      3100      3110      3120

1326258      140      150
GCACTTTCCTCCTCTGTGCTCT
      ** ** ** ***** :
hpatched     GCGCTGTCTTCCTTCTGAACCC
      3130      3140

```

```

1326258      10      20      30      40      50
CCGGGCAGCATGCGCAGAGGCCGGCCAGGCTGGGGTGCACGCCTACCCCA
      ***** ***** * * * * * * * * * * :
hpatched.RC  CCGGGCGGCATG--GCGAAGCGGACCAAGCTGGGGGGTGGCTCAGGGGAG
      710      720      730      740      750

```


**FIG. 2B**

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PTCH 1 MASAGNAAEPODRGGGGGCGICAGPRPAGGRRRTTGLRRAA[PDRDYL  
PTCH2 1 .....MTRSPPLREL.

PTCH 51 HRPSYCDAAFALEQISKGKA[TKRKAPLWLRK][FQRL][F][K][G][C][Y][I][K][N][C][G][K]  
PTCH2 11 .PPSYTPP..[ARTAAPQIL][AGSL][KAPLWLRAY][FQGL][FSLGCGI][QRHCGK]

TM1

PTCH 101 F[V][V][G][L][I][F][G][A][F][A][V][G][L][K][A][A][N][L][E][T][N][V][E][E][L][W][V][E][V][G][G][R][V][S][R][E][L][N][Y][T][R][Q][K][I][G][E][E]  
PTCH2 58 V[F][F][G][L][I][F][G][A][F][A][V][G][L][K][A][A][N][L][E][T][N][V][E][E][L][W][V][E][V][G][G][R][V][S][R][E][L][N][Y][T][R][Q][K][I][G][E][E]

PTCH 151 A[M][F][N][P][Q][L][M][I][Q][T][P][K][E][G][A][N][V][L][T][T][E][A][L][L][Q][H][L][D][S][A][L][Q][A][S][R][V][H][V][M][Y][N][R][Q][W][K][L][E]  
PTCH2 108 AAYTSQMLIQ[TA][R][Q][E][G][E][N][I][L][T][P][E][A][L][G][L][H][L][Q][A][L][T][A][S][K][V][Q][V][S][L][Y][G][K][S][W][D][L][N]

PTCH 201 HLCYKSGELIT[ETGYMDQII][EYLYPCLI][ITPLDCFWEGAKLQSGTAYLLG  
PTCH2 158 KICYKSGVPLI[ENGMI[EWMI][EKL][FPCV][IL][TPLDCFWEGAKLQSGTAYLLG]

PTCH 251 K[P][P][L][R][W][T][N][F][D][P][L][E][F][L][E][E][L][K][K][I][N][Y][Q][V][D][S][W][E][E][M][L][N][K][A][E][V][G][H][G][Y][M][D][R][P][C][L][N][P][A]  
PTCH2 208 R[P][D][I][Q][W][T][N][L][D][P][E][Q][L][L][E][E][L][G][P][F][A][S][L][E][G][F][R][E][L][L][D][K][A][Q][V][G][Q][A][Y][V][R][P][C][L][H][P][D]

PTCH 301 [D][P][D][C][P][A][T][A][P][N][K][N][S][T][K][P][L][D][M][A][L][V][L][N][G][G][C][H][G][L][S][R][K][Y][M][H][W][Q][E][E][L][I][V][G][G][T][V][K][N][S]  
PTCH2 257 [D][L][H][C][P][P][S][A][P][N][H][H][S][R][Q][A][P][N][V][A][H][E][L][S][G][G][C][H][G][F][S][H][K][F][M][H][W][Q][E][E][L][L][G][G][M][A][R][D][P]

FIG.--3A

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PTCH 351	TGK	L	V	S	A	H	A	L	Q	T	M	F	Q	L	M	T	P	K	Q	M	Y	E	H	F	K	G	Y	E	V	S	H	I	N	W	N	E	D	K	A	A	I	L	E	A	W					
PTCH2 307	Q	G	E	L	L	R	A	E	A	L	Q	S	T	F	L	L	M	S	P	R	Q	L	Y	E	H	F	R	G	D	Y	Q	T	H	D	I	L	G	M	S	E	E	Q	A	S	T	V	L	Q	A	W
TM2																																																		
PTCH 400	Q	R	T	Y	V	E	V	H	Q	S	V	A	Q	N	S	T	Q	K	V	L	S	F	T	T	T	T	L	D	D	I	L	K	S	F	S	D	V	S	V	R	V	A	S	G	Y	L	L	M		
PTCH2 356	Q	R	R	F	V	Q	L	A	Q	E	A	L	P	E	N	A	S	Q	I	H	A	F	S	S	T	T	L	D	D	I	L	H	A	F	S	E	V	S	A	A	R	V	V	G	Y	L	L	M		
TM3																																																		
PTCH 450	L	A	Y	A	C	L	T	M	L	R	W	D	C	S	K	S	Q	G	A	V	G	L	A	G	V	L	L	V	A	L	S	V	A	A	G	L	G	L	C	S	L	I	G	I	S	F	N	A	A	T
PTCH2 406	L	A	Y	A	C	V	T	M	L	R	W	D	C	A	Q	S	Q	G	S	V	G	L	A	G	V	L	L	V	A	L	A	V	A	S	G	L	G	L	C	A	L	L	G	I	T	F	N	A	A	T
TM4																																																		
PTCH 500	T	Q	V	L	P	F	L	A	L	G	V	C	V	D	D	V	F	L	L	A	H	A	F	S	E	T	G	Q	N	K	R	I	P	F	E	D	R	T	G	E	C	L	K	R	T	G	A	S	V	
PTCH2 456	T	Q	V	L	P	F	L	A	L	G	I	C	V	D	D	V	F	L	L	A	H	A	F	T	E	A	L	P	G	--	T	P	L	Q	E	R	M	G	E	C	L	Q	R	T	G	T	S	V		
TM5																																																		
PTCH 550	L	T	S	I	N	V	T	A	F	F	M	A	A	L	I	P	I	P	A	L	R	A	F	S	L	Q	A	A	V	V	V	F	N	F	N	F	A	M	V	L	L	I	F	P	A	L	L	S	M	
PTCH2 504	L	T	S	I	N	M	A	A	F	L	M	A	A	L	V	I	P	A	L	R	A	F	S	L	Q	A	A	I	V	V	G	C	T	E	V	A	V	M	L	V	F	P	A	L	L	S	L			
TM6																																																		
PTCH 600	L	Y	R	R	E	D	R	R	L	D	I	F	C	C	F	T	S	P	C	V	S	R	V	I	Q	V	E	P	Q	A	Y	T	D	T	H	D	N	T	R	Y	S	P	P	P	P	Y	S	S	H	
PTCH2 554	L	R	R	R	H	C	Q	R	L	D	V	L	C	C	F	S	S	P	C	S	A	Q	V	I	Q	I	L	P	Q	E	L	G	D	G	T	.....	V	P	V	G										
TM7																																																		
PTCH 650	F	A	H	E	T	Q	I	T	M	Q	S	T	V	Q	L	R	T	E	Y	D	P	H	T	H	V	Y	T	T	A	E	P	R	S	E	I	S	V	Q	P	V	T	V	T	Q	D	T	L	S		
PTCH2 593	I	A	H	.....	L	T	A	T	V	Q	A	F	T	H	C	E	A	S	S	Q	H	V	T	I	L	P	Q	A	H	L	V	P	P	.....	S	D	P	L	G											

FIG.-3B

PTCH 700 QSPESTSSTRDLLSQFSDSSLH..CLEPPCTKMTLSSFAEKHYAPFLKPP  
PTCH2 634 ELFSPPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLQS

TM7

PTCH 748 KAK VVV VFL FLGLGV SLYGTTRVRDGLDLTDIVPRETREYDFIAAQFKV  
PTCH2 684 HAK A HVL VLFGLGLGL SLYCATLVQDGLALTDVVPRTKEHAFLSAQLRY

PTCH 798 FSFY NMYIVTQKA - DYPNIQHLLYDLHRSFSNVK YVLMLEENKQLPKMWLH  
PTCH2 734 FSLYEALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPATQAPRTWLH

\*\*\*

PTCH	847	YF	RD	WL	QG	LQ	DA	FD	SD	WE	TK	IM	PN	NY	KN	GS	DD	GV	LAY	KLL	VQ	TG	SR	DK	IP	
PTCH2	784	YY	RN	WL	QG	LQ	DA	FD	QD	WA	SG	RI	TR	HS	YR	NG	SE	ED	GA	LAY	KLL	IQ	TG	DA	QE	IP

PTCH 897 ID ISQLTKQR[LVD]ADGIINIPSAFYIYLTAWVNSDPVAYAAASQANIRPHRP  
PTCH2 834 LD FSQLTTRK[LVD]REGLLIPPELFYMGLTVVWSSDPLGLAAASQANFYPPPP

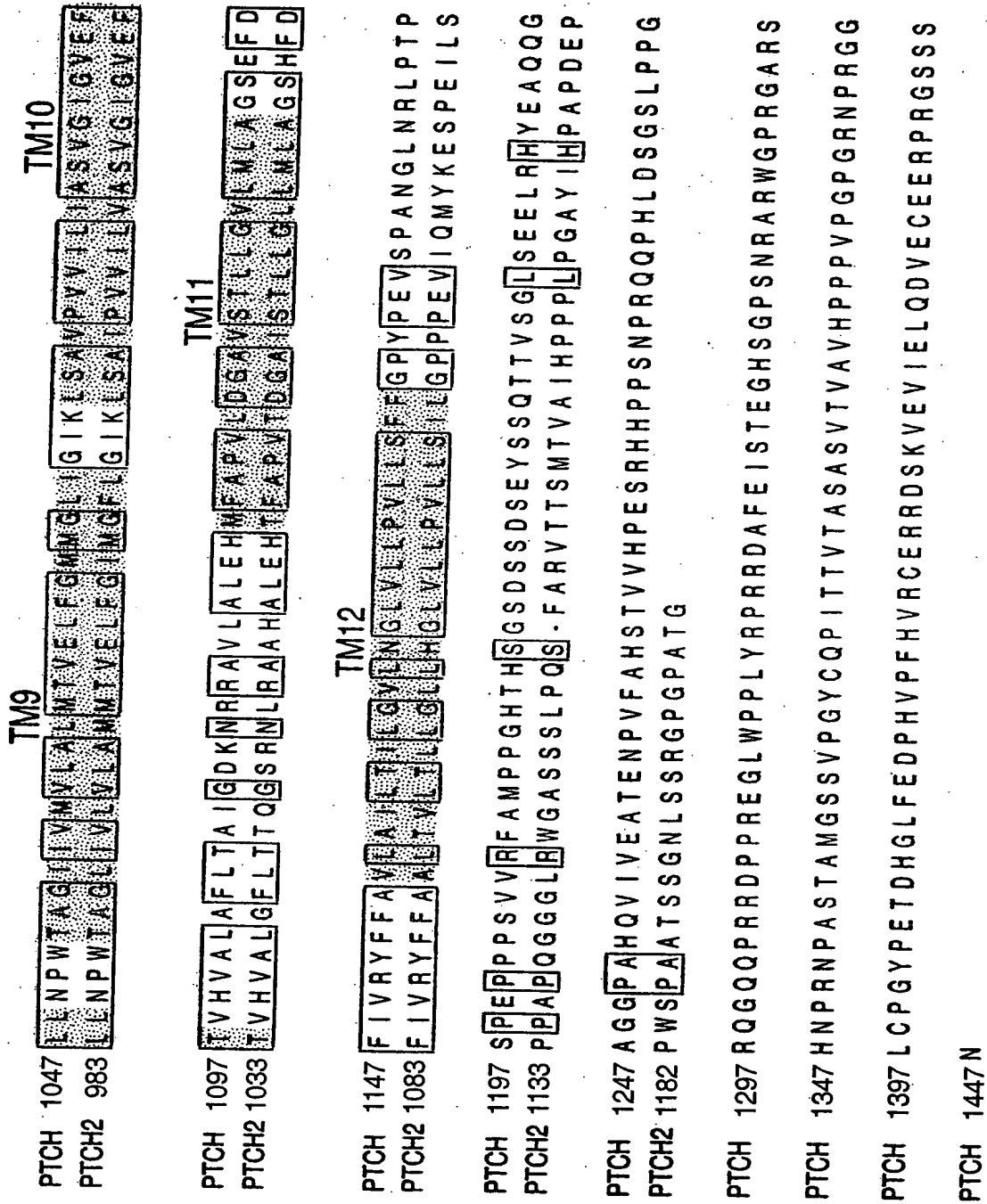
PTCH 947 EWVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDLTSDFVEAIEKVIRT  
PTCH2 884 EWLHDKYD.TTGENLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARIA

TM8

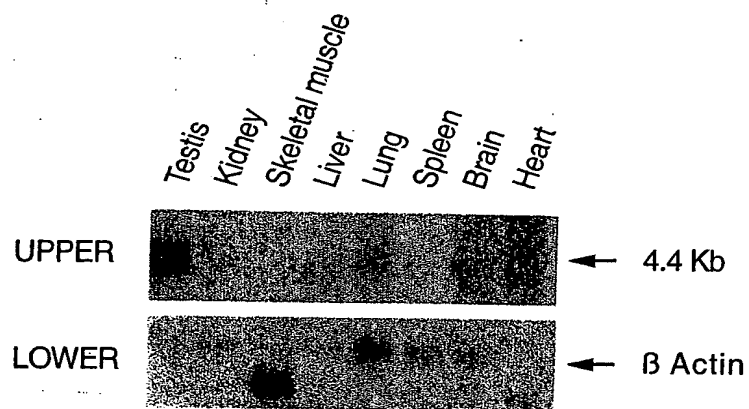
PTCH 997 IC SN Y T S L G L S S Y P N G Y P P F L F W E Q Y I G L R H W L L F S V V L A C T F L V C A V F  
PTCH2 933 A C A E A G Q A G V H A Y P S G S P P F L F W E Q Y L G L R R C F L A V C I L L V C T F L V C A L L

**FIG. 3C**

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**FIG.--3D**

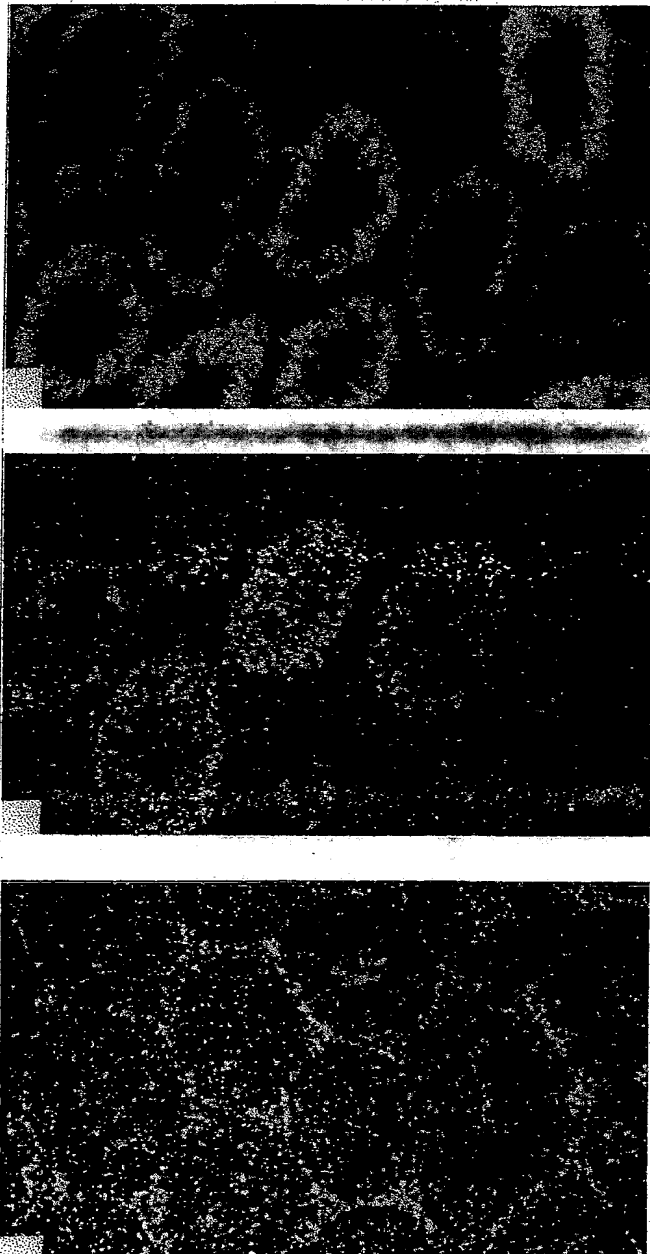
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**FIG.\_4**



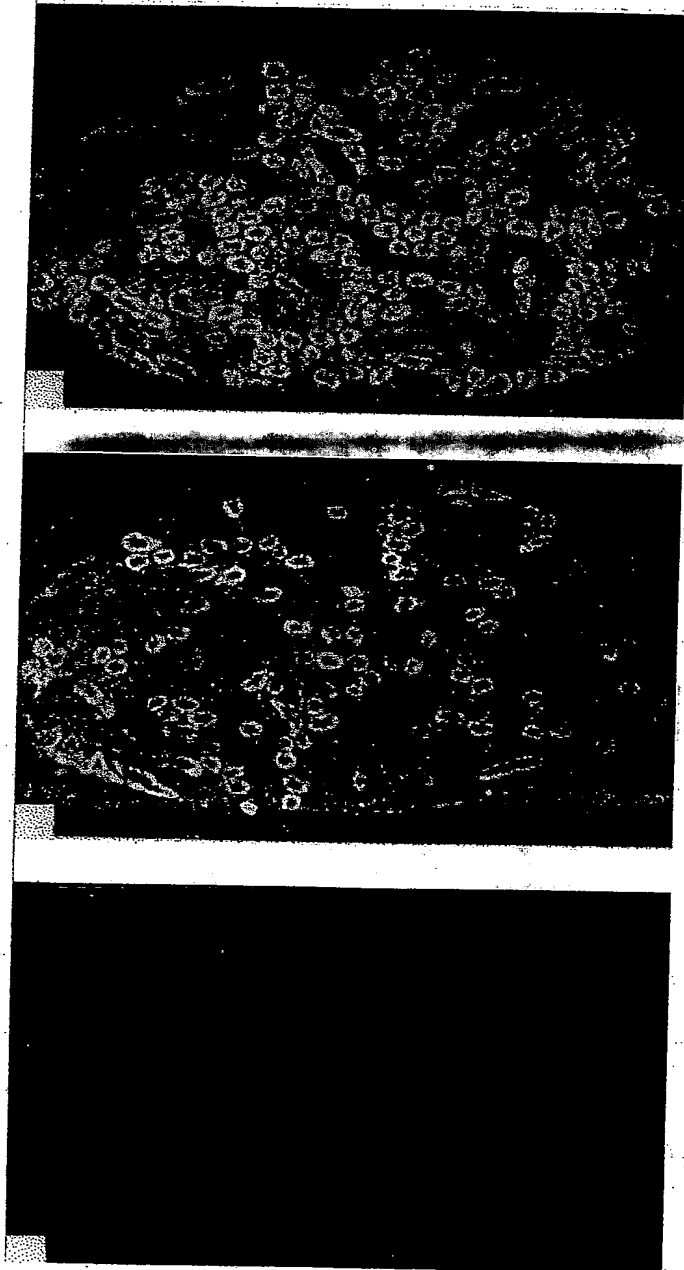
**FIG.\_5**



**FIG.\_6A**

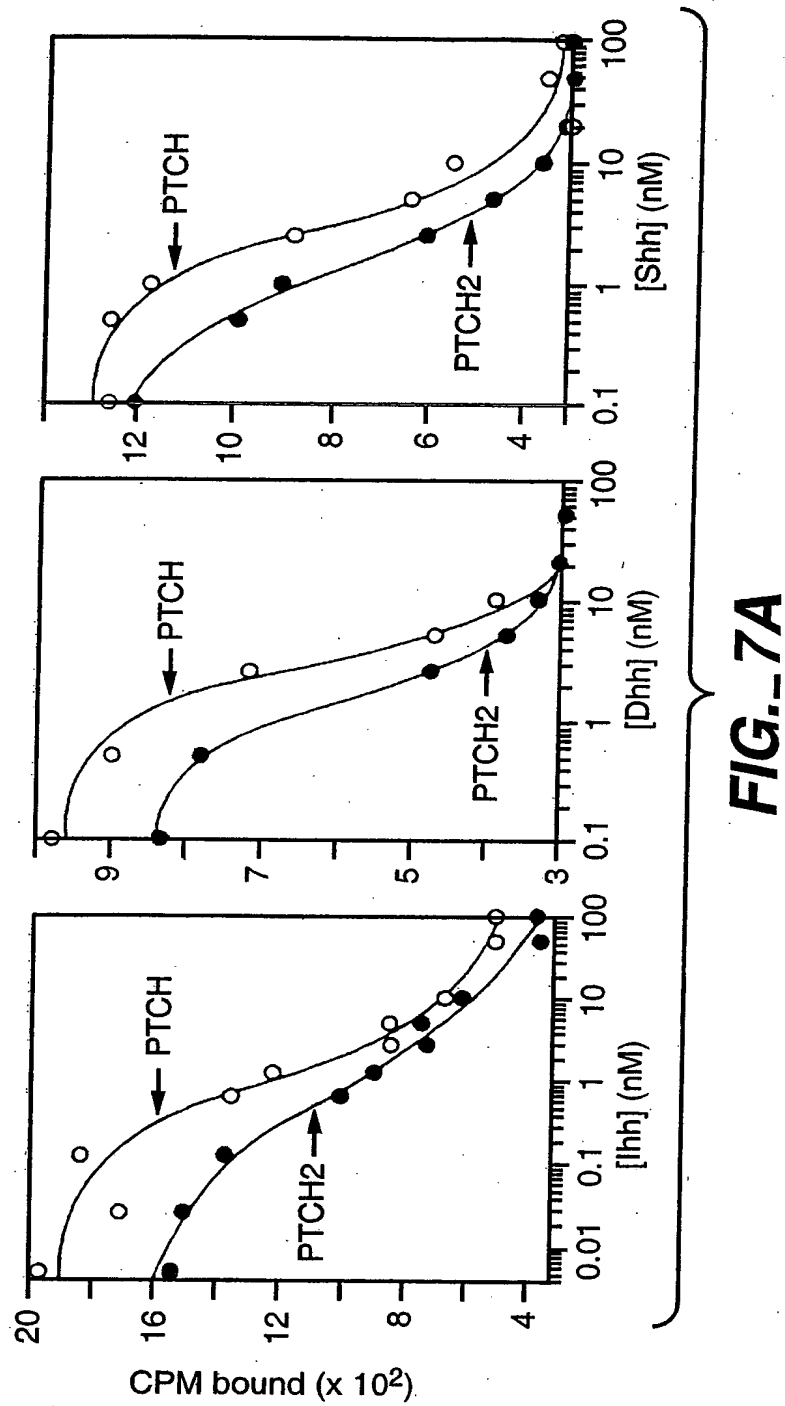
**FIG.\_6B**

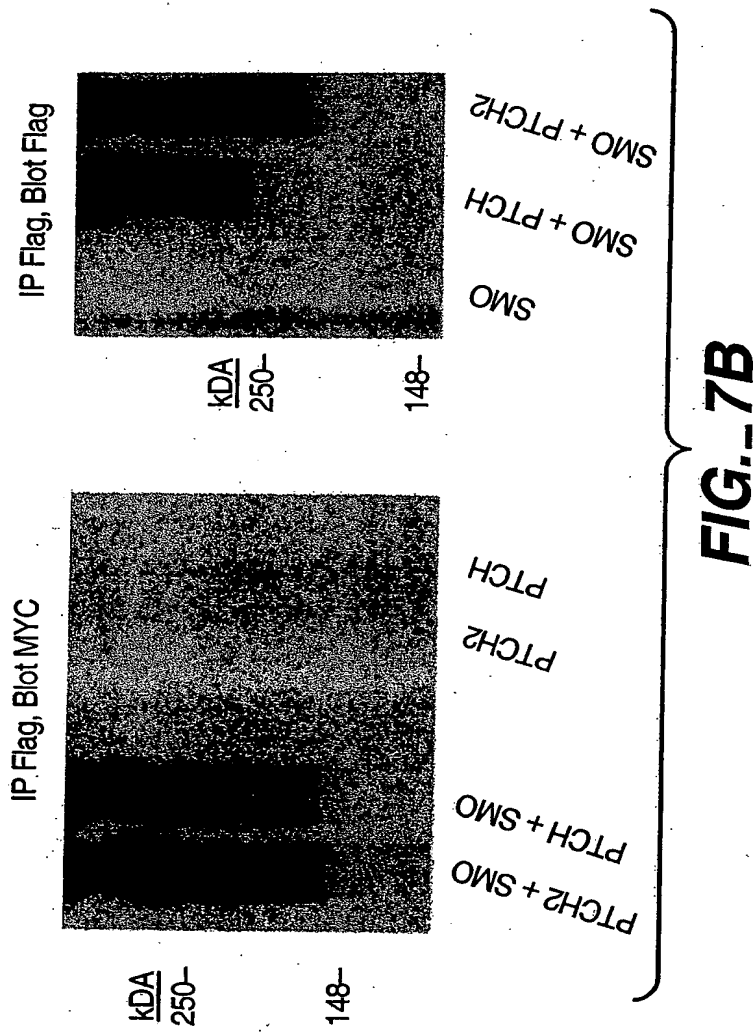
**FIG.\_6C**



**FIG.\_6D** **FIG.\_6E** **FIG.\_6F**

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**FIG. 7A**

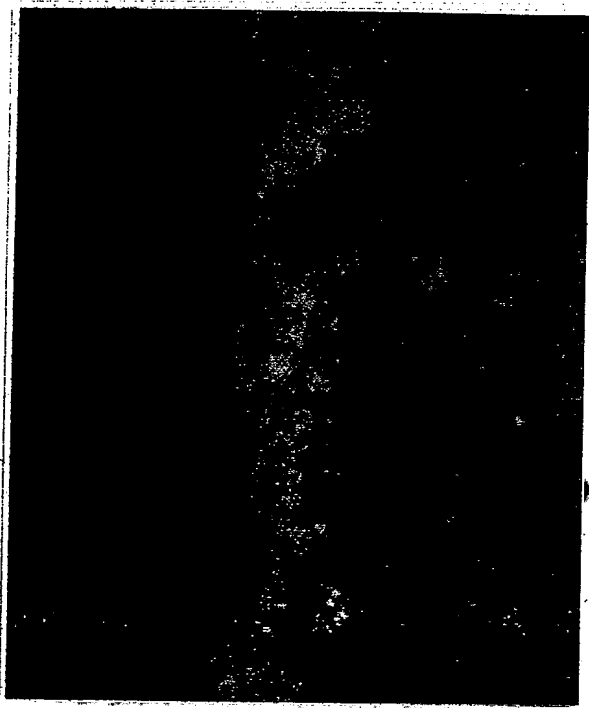


	10	20	30	40	50
hPitch-2	MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGGLLFSLGCG				
mPatched2	MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGGLLFSLGCR				
	10	20	30	40	50
	60	70	80	90	100
hPitch-2	IQRHCGKVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYT				
mPatched2	IQKHCGKVLFLGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYT				
	60	70	80	90	100
	110	120	130	140	150
hPitch-2	KEKLGEAAAYSQM LIQTARQEGENILTPEALGLHLQAALTASKVQVSLY				
mPatched2	KEKLGEAAAYSQM LIQTAHQEGGNVLTPEALDLHLQAALTASKVQVSLY				
	110	120	130	140	150
	160	170	180	190	200
hPitch-2	GKSWDLNKICYKSGVPLIENGMI EWMI EKLFPCVILT PLDCFWEGAKLQG				
mPatched2	GKSWDLNKICYKSGVPLIENGMI ERMIEKLFPCVILT PLDCFWEGAKLQG				
	160	170	180	190	200
	210	220	230	240	250
hPitch-2	GSAYLPGRPD IQWTNLDP EQLL EELGP FASLEG FRELLDKAQVGQAYVGR				
mPatched2	GSAYLPGRPD IQWTNLDP QQLLEELGP FASLEG FRELLDKAQVGQAYVGR				
	210	220	230	240	250
	260	270	280	290	300
hPitch-2	PCLHPDDLHC PPSAPNHHSRQ APNV AHEL SGGCHGF SHKF MHWQEELL LG				
mPatched2	PCLDPDDPHC PPSAPNRHSRQ APNV AQEL SGGCHGF SHKF MHWQEELL LG				
	260	270	280	290	300
	310	320	330	340	350
hPitch-2	GMARD PQGELLRAEALQSTFLLMS PRQLYEHFRGDYQTHDIGWSEEQAST				
mPatched2	GTARD LQGQLLRAEALQSTFLLMS PRQLYEHFRGDYQTHDIGWSEEQASM				
	310	320	330	340	350

**FIG. 8A**



PTCH2



PTCH

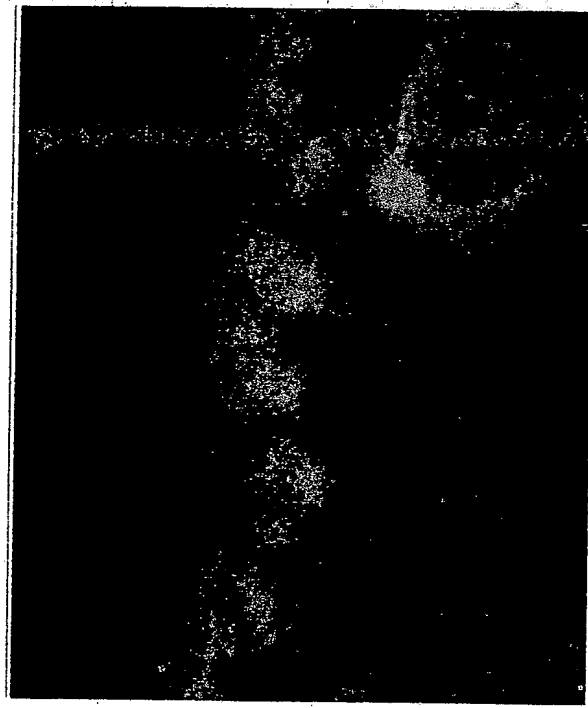


FIG. 9

1 CCCACGGCTC CGGGAGAAGC TGGGGGAGGA GGCTGCATAC ACCTCTCAGA TGCTGATACA GACCGCAGGC CAGGAGGAG AGAACATCCT CACACCCGAA  
GGGTGGCAG GCCCTCTTCG ACCCCCTCCT CCGACGTATG TGGAGAGTCT ACGACTATGT CTGGCGTGG GTCTCCCTC TCTTGTAGGA GTGTGGGCTT

101 GCACTTGGCC TCCACCTCCA GGCAGCCCTC ACTGCCAGTA AAGTCCAAGT ATCACTCTAT GGAAGTCCT GGAATTGAA CAAATCTGC TACAAGTCAG  
CGTGAACCG AGGTGGAGGT CCGTCGGGAG TGACGGTCTAT TTCAGGTTC TAGTGAGATA CCCTTCAGGA CCCTAAACTT GTTTTAGACG ATGTTCAGTC

201 GAGTCCCTT TATTGAAAAT GGAATGATTG AGCGGATGAT TGAGAAGCTG TTTCCGTGCG TGATCCTCAC CCCCTCGAC TGCTTCTGGG AGGGAGCCAA  
CTCAAGGGGA ATAACTTTTA CCTTACTAAC TCGCCTACTA ACTCTTCGAC AAAGGCACGC ACTAGGAGTG GGGGAGCTG ACGAAGACCC TCCCTCGGTT

301 ACTCCAAGG GGTCCGCT ACCTGCCGCT CCCAATGTGG CTCACGAGCT GAGTGGGGC TGCCATGGCT TCTCCACAA ATTCTGCAC TGGCAGGAGG  
TGAGGTTCCC CCGAGGCGGA TGGACGGCGA GGGTTACACC GAGTGCTCGA CTCACCCCCG ACGGTACCGA AGAGGTGTT TAAGTAGTG ACCGTCCTCC

401 AATTGCTGCT GGGAGGCATG GCCAGAGACC CCCAAGGAGA GCTGCTGAGG GCAGAGGCC GCAGAGCAC CTTCTTGCTG ATGAGTCCC GCCAGCTGTA  
TTAAGCAGCA CCTCCGTAC CGTCTCTGG GGGTTCCTCT CGACGACTCC CGTCTCCGG ACGTCTCGTG GAAGAACGAC TACTCAGGG CGGTGACAT

501 CGAGCATTC CGGGTGACT ATCAGACACA TGACATTGGC TGGAGTGAGG AGCAGGCCAG CACAGTGCTA CAAGCCTGGC AGCGGCGCTT TGTGCAGGTC  
GCTCGTAAAG GCGCCACTGA TAGTCTGTGT ACTGTAACCG ACCTCACTCC TCGTCCGGTC GTGTACAGAT GTTCGGACCG TCGCCGCGAA ACACGTCCAG

601 GGTATGGACA AGGACAGGG GGTGCCCTGA GGCCATTCCC TCTCTCTGCC CCTCTCTATC CACCTGTTT CTCCAGCTGG CCCAGGAGGC CCTGCTGAG  
CCATACCTGT TCCTGTCCCC CCACGGGACT CCGGTAAGG AGGAGGACGG GGGAGGATAG GTGGGACAAA GAGGTGACCG GGTCTCTCCG GGACGGGACT

FIG. 10A

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701 AACGCTTCCC AGCAGATCCA TGCCCTTCTCC TCCACCACCC TGGATGACAT CCTGCATGCG TTCTCTGAAG TCAGTGCTGC CCGTGTGGTG GGAGGCTATC  
TTGCGAAGGG TCGTCTAGGT ACGGAAGAGG AGGTGGTGGG ACCTACTGTA GGACGTACGC AAGAGACTTC AGTCACGACG GGCACACCAC CCTCCGATAG

801 TGCTCATGGT GGGTCTTGCA CCTGGCACT TGCCCCCACC CCACCTCCAA CCAGTGCCCA CCCTGGGAG CCCCTGAGAC TGCCCTTTCC CCCCACAGCT  
ACGAGTACCA CCCAGAACGT GGACCGTGGA ACGGGGGTGG GGTGGAGGT GGTACAGGGT GGGACCCCTC GGGGACTCTG ACGGGAAGG GGGGTGTGGA

901 GGCCTATGCC TGCTGCGTG GGA CTGCGCC CAGTCCCAGG GTTCCGTGG CCTTGCCGG GTACTGCTGG TGGCCCTGGC GGTGGCCCTCA  
CCGGATACGG ACACACTGGT ACGACGCCAC CTTGACGCGG GTCAGGTCC CAAGGCACCC GGAACGGCCC CATGACGACC ACCGGGACCG CCACCGGAGT

1001 GGCCTTGGC TCTGTGCCCT GCTCGGCATC ACCTTCAATG CTGCCACTAC CCAGGTACGC CAGGACTGCA GGGCAGACTC AGTGCCAGTC ACCAGGCTTC  
CCGGAACCCG AGACACGGGA CGAGCCGTAG TGAAGTTAC GACGGTGATG GTCCATGCG GTCCCTGACGT CCCGTCTGAG TCACGGTCTAG TGGTCCGAAG

1101 ACGGTCCTC AGTGCCCGC TCCTCTGCC CTCCAGGTGC TGCCCTTCTT GACTCTGGA ATCGGCGTGG ATGACGTATT CCTGCTGGCG CATGCCCTCA  
TGCCCAAGGAG TCGACGGGCG AGGAGACGGG GAGGTCCACG ACGGGAAGAA CTGAGACCCT TAGCCGCACC TACTGCATAA GGACGACCGC GTACCGAAGT

1201 CAGAGGCTCT GCCTGGCACC CCTCTCCAGG TGGGGCCTTG TCCCCCAGG CTCATCTGAG GCAGCTCAGC TTA CTGGTTA AGAGCCTCTT GGTTCAGTG  
GTCTCCGAGA CGGACCGTGG GGAGAGGTCC ACCCCGGGAC AGGGGGTCCC GAGTAGACTC CGTCGAGTCG AATGACCAAT TCTCGGAGAA CCAAGTTTAC

1301 ACCTTGGGCT GCTAATGAAC CTCGGTGCCT CTTGTCCCA TGTGTAAACA GGGAAATAA TAGTGTGTG TCCTAAGGT TATTGTTGG ATCAGTGAAG  
TGGAAACCGA CGATTACTTG GAGCCACGGA GAACAGGGT ACACATTTGT CCCCTTTATT ATCAGACAC AGGATTCCCA ATAACAACCC TAGTCATTC

1401 TAACTCAAGT TGAATGCTTA GAACAGCCCC TCATACGTAC ATGGTACCA ATAAATGCTA GCCACTGTGT TATGACTGCC CCACCTCTGC ACCCCAAGTT  
ATTGAGTTCA ACTTACGAAT CTTGTGGGT AGTATGCATG TACCATGGGT TATTACCAT CCGTGACACA ATACTGACGG GGTGGAGACG TGGGGTTCAA

FIG.-10B

1501 CCTGAGCCTC CCCTTCACTC CACTTTGACA CGGCCCTCTC CTTGTGACCT GAGGCAGGT CCCCACTCTG TCCTGGCAGG AGCGCATGGG CGAGTGTCTG  
GGACTCGGAG GGGAACTGT GTGAACTGT GCGGGGAGG GAACACTGGA CTCCTGTCGA GGGGTGAGAC AGGACCGTCC TCGGTATACC GCTCACAGAC

1601 CAGCGCAGG GCACCACTGT TGTACTACA TCCATCAACA ACATGGCCGC CTTCTCTCATG GTTGCCTCG TTCCCATCCC TCGGCTGCGA GCCTTCTCCC  
GTCGCGTGCC CGTGGTCACA ACATGAGTGT AGGTAGTTGT TGTACCGGCG GAAGGAGTAC CGACGGGAGC AAGGTTAGG ACGCACGCT CGGAAGAGGG

1701 TACAGCCTGG ACCTACGGG GCGCCACTGC CAGGCCCTTG ATGTGCTCTG CTGCTTCTCC AGGTACTGCC TCGGCCCCAG CCCCTTCTC CCGTGACCCA  
ATGTGGACC TGGATGCCGC CGCGGTGACG GTCGCGGAAC TACACGAGAC GACGAAGAGG TCCATGACGG ACGCGGGGTC GGGGAAGGAG GGCATGGGT

1801 CGCCAGCCTG TCCCCTCACC AGCATTTCOA GGCACAGACC TGTCTACCTC TTCCAGTCCC TGCTCTGCTC AGGTGATTCA GATCTGCCCC  
GCGGTGGGAC AGGGGAGTGG TCGTAAAGTT CCGTGTCTGG ACAGTAGGTG AGAGATGGAG AAGGTCAGG ACGAGACGAG TCCACTAAGT CTAGGACGGG

1901 CAGGAGCTGG GGGACGGGAC AGTACCACTG GGCATTGCCC ACTCACTGC CACAGTTCAA GCCTTTACCC ACTGTGAAGC CAGCAGCCAG CATGTGGTCA  
GTCCTCGACC CCTGCCCCG TCATGGTTCAC CCGTAACGGG TGGAGTGACG GTGTCAAGTT CGGAATGGG TGACACTTCG GTCGTGCTC GTACACCAGT

2001 CCATCTCTGC TCCCAAGCC CACCTGGTGC CCCCACCTTC TGACCCACTG GGTCTGAGC TCTTCAGCCC TGGAGGTCC ACACGGGACC TTCTAGGCCA  
GGTAGGACGG AGGGTTCTGG GTGGACCACG GGGGTGGAAG ACTGGGTGAC CCGAGACTCG AGAAGTGGG ACCTCCGAGG TGTGCCCTGG AAGATCCGGT

2101 GGAGGAGGAG ACAAGGCAGA AGGCAGCCTG CAAGTCCCTG CCTGTGCCC GGTGGAATCT TGCCCATTTT GCGCGCTATC AGTTTGCCCC GTTGTGCTC  
CCTCCTCCTC TGTTCGGTCT TCCGTGCGAC GTTCAGGGAC GGCACACGGG GCACCTTAGA ACGGTTAAG CCGGGCATAG TCAACGGGG CAACGACGAG

2201 CAGTCACATG CCAAGGCCAT CGTGTGGTGG CTCTTCTGGG CTTGAGCCTC TACGGAGCCA CCTTGTGCA AGACGGCCTG GCCCTGACGG  
GTCAGTGTAC GGTTCGGTA GCACGACCAC GAGAAACCAC GGAAGACCC GGAAGTGGG ATGCTCGGT GGAACACGCT TCTGCCGGAC CGGGAAGTGG

**FIG. 10C**

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2301 ATGTGGTGCC TCGGGGCACC AAGGAGCATG CCTTCCTGAG CGCCACAGTC AGTACTTCT CCTGTACGA GGTGGCCCTG GTGACCCAGG GTGGCTTTGA  
TACACCACGG AGCCCGGTGG TTCTCTGTAC GGAAGGACTC GCGGTCGAG TCCATGAAGA GGGACATGCT CCACCGGGAC CACTGGGTCC CACCGAAACT

2401 CTACGCCCCA TCCCAACGGC CCCTCTTTGA TCTGCACCAG CGCTTCAGTT CCTCAAGGC GGTGCTGCCC CCACCGGCCA CCCAGGCACC CCGCACCTGG  
GATCGGGTG AGGGTGGCG GGGAGTGGC AGACGTGGTC GCGAAGTCAA GGGAGTTCCG CCACGACGGG GGTGCCGGT GGTGCCGTGG GCGGTGGACC

2501 CTGCACTATT ACCGCAACTG GCTACAGGGA ATCCAGGCTG CCTTTGACCA GGAAGTGGT TCTGGGCGCA TCACCCGCCA CTCGTACCGC AATGGTCTG  
GACGTGATAA TGGCGTTGAC CGATGTCCCT TAGGTCCGAC GGAAACTGGT CCTGACCCGA AGACCCGGT AGTGGCGGT GAGCATGGCG TTACCGAGAC

2601 AGGATGGGC CCTGGCCTAC AAGTGCTCA TCCAGACTGG AGACGCCAG GAGCCTCTGG ATTTACGCCA GGTGGGAGA GGGCTGGAGG GGTCCACTAG  
TCCTACCCCG GGACCGGATG TTGACGAGT AGGTCTGACC TCTGCGGTC CTCGGAGACC TAAAGTCGT CCAACCTCT CCCGACCTCC CCAGGTGATC

2701 TACAGGGGT GCAGGCCTCC TGGGCCCAGG CCTTCAGCCC TCTTGCCCTC TGCAGCTGAC CACAAGGAAG CTGGTGGACA GAGAGGGAAT GATTCACCC  
ATGTCCCGA CGTCCGGAGG ACCCGGGTCC GGAAGTCGG AGAGACGGAG AGTCGACTG GTGTTCTTC GACCACCTGT CTCTCCCTGA CTAAGGTGGG

2801 GAGCTCTTCT ACATGGGGCT GACCGTGTGG GTGAGCAGTG ACCCCCTGG TCTGGCAGCC TCACAGGCCA ACTTCTACCC CCCACCTCCT GAATGGCTGC  
CTCAGAAGA TGTACCCCGA CTGGCACACC CACTCGTCAC TGGGGGADCC AGACCGTCGG AGTGTCGGT TGAAGATGG GGGTGGAGA CTTACCGACG

2901 ACGACAAATA CGACACCAG GGGGAGAACC TTCCAGTGA GTCTTGGGG GAGTCGGCA AGAGCCTCAG CCTCGCCAC ACAAGCCCTG AGCCTGAGGC  
TGCTGTTTAT GCTGTGTGTC CCCCTCTTGG AAGCGTCACT CAGAACCCCT CTCGAGCGT TCTCGGAGTC GGAGCGGTG TGTTCGGGAC TCGGACTCCG

3001 CCTGCCCCACT CTGCCCGGTG CTCACCGCCC TGTCCCTCTC CCTCTTCTCC CTTCCCTCC CCTCCACAGT CCCGCCAGT CAGCCCTGG AGTTTGCCCA  
GGACGGGTGA GACGGGCAC GAGTGGCGG ACAGGGAGAG GGAGAAGAG GAAGGGAGG GGAGTGTCA GGGCGGTCA GTCGGGAACC TCAACGGGT

FIG. 10D

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3101 GTTCCCTTC CTGCTGGTG GCCTCCAGAA GACTGCAGAC TTGTGGAGG CCATCGAGGG GGCCCGGGCA GCATGCGCAG AGGCCGGCCA GGCTGGGGTG  
 CAAGGGGAAG GACGACGCAC CGGAGGTCTT CTGACGTCTG AATACACTCC GGTAGCTCC CCGGCCCCGT CCGGCCCCGT CCGACCCCCAC  
 3201 CACGCCTACC CCAGCGGCTC CCCCTTCCTC TTCTGGGAAC AGTATCTGG CCTGGGGGC TGCTTCCTGC TGGCCGTCTG CATCCTGCTG GTGTGCACCTT  
 GTGCGGATGG GGTGCGCCGAG GGGGAAGGAG AAGACCTTG TCATAGACCC GGACGCCGG ACAGGAGAG ACCGGCAGAC GTAGGACGAC CACACGTGAA  
 3301 TCCTCGTCTG TGCTCTGCTG CTCCTCAACC CCTGGACGGC TGGCCTCATA GTGAGTGCTT GCAGGAGTGG GGACAGAGAC ACCCCACCTT TCCCTGCCCA  
 AGGAGCAGAC ACGAGACGAC GAGGAGTTGG GGACCTGCCG ACCGGAGTAT CACTCAGAA CTCCTCACC CCTGTCTCTG TGGGTGGA AGGGACGGGT  
 3401 GCCTGTCTC CCTCCTGCCA GGAGCCCTCT GTGAGCCCTG TCTCCCTCAG GTGCTGTCTG TGGCATGAT GACAGTGGAA CTCCTTTGGTA TCATGGGTTT  
 CGGACAGTAG GGAGGACGGT CCTCGGGAGA CACTCGGGAC AGAGGGAGTC CACGACCAGG ACCGCTACTA CTGTCACTT GAGAAACCAT AGTACCCAAA  
 3501 CCTGGGCATC AAGCTGAGTG CCATCCCGT GGTGATCCTT GTGGCCTCTG TAGGCATTGG CGTTGAGTTC ACAGTCCAG TGGCTCTGGT GAGCAGGGC  
 GGACCCGCTAG TTCGACTCAC GGTAGGGGCA CCACTAGGAA CACCGGAGAC ATCCGTAACC GCAACTCAAG TGTCAGGTGC ACCGAGACCA CTCGTGCCCCG  
 3601 ACCCCGGGGA GGGACCAATC AGCTGATTCA GTATTCAACA CATATTGTTT AAGCCCTAC TATGTGCTAG GTACTATTTA AGAATTGGG CTGGGTGGAC  
 TGGGGCCCT CCCTGGTTAG TCGACTAAGT CATPAAGTTGT GTATAACAAG TTCGGGGATG ATACACGATC CATGATAAAT TCTTAAACCC GACCCACCTG  
 3701 GTGGTGGCTC ATTCTGTAA TCCCAGCACT TTGGGAGGCC GAGGCGGGTG GATCACCTGA GGTCGGGAGT TCGAAACCAG CCTGGCCAAC ATGTGAAAC  
 CACCACCGAG TAAGGACATT AGGGTCGTGA AACCTCCGG CTCGGCCAC CTAGTGGACT CCAGCCCTCA AGCTTTGGTC GGACCGGTTG TACCACTTG  
 3801 CCTGTCTTTA CTAATAATAC AAAAAATTAG CCAGGCGTGG TGGCACATGC CAGTAGTCCC AGCTACTTTG GAGGCTGAGG CAGAATTGCT TGAACCTGGG  
 GGACAGAAAT GATTTTATG TTTTAAATC GGTCCGCACC ACCGTGTACG GTCATCAGG TCGATGAAAC CTCGACTCC GTCTTAAAGA ACTTGGACCC  
 3901 AGGCGAAGT TGCAGTGAGC TGAGATCGTG CCATTGCACT CCAGCTGGG CAACAAGAGT GCAACTCTCC GTCTCAAAA AAAAAAAA AAGGGCGGCC  
 TCCGCTTCCA AGTCACTCG ACTCTAGCAC GGTAACGTGA GGTGCGACCC GTTGTCTCA CGTTGAGAGG CAGAGTTTTT TTTTTTTTTT TTCCCGCCGG  
 4001 GCGA  
 CGCT

FIG.-10E

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1 TTCCGGCATG ACTCGATCGC CGCCCTCAG AGAGCTGCCC CCGAGTTACA CACCCCCAGC TCGAACCGCA GCACCCACAGA TCCTAGCTGG GAGCCTGAAG  
AAGGCCGTAC TGAGCTAGCG GCGGGAGTC TCTCGACGGG GGCTCAATGT GTGGGGGTG AGCTTGGCGT CGTGGGTCT AGGATCGACC CTCGGACTTC

101 GCTCCACTCT GGCTTCGTGC TTAATTCCAG GGCCTGCTCT TCTCTCTGGG ATGCGGATC CAGAGACATT GTGGCAAGT GCTCTTTCTG GGACTGTTGG  
CGAGGTGAGA CCGAAGCAGC AATGAAGTC CCGGACGAGA AGAGAGACCC TAGCCCTAG GTCTCTGTAA CACCGTTTCA CGAGAAAGAC CCTGACAACC

201 CCTTTGGGGC CCTGGCATTG GGTCTCCGCA TGGCCATTAT TGAGACAAAC TTGGAACAGC TCTGGGTAGA AGTGGGCAGC CGGGTGAGCC AGGAGCTGCA  
GGAAACCCCG GGACCGTAAT CCAGAGGCGT ACCGGTAATA ACTCTGTTG AACCTTGTCG AGACCCATCT TCACCCGTCG GCCCACTGG TCCTCGACGT

301 TTACACCAAG GAGAAGCTGG GGGAGGAGGC TGCATACACC TCTCAGATGC TGATACAGAC CGCAGGCCAG GAGGGAGAGA ACATCCTCAC ACCCGAAGCA  
AATGTGGTTC CTCTTCGACC CCTCCTCCG ACGTATGTGG AGAGTCTACG ACTATGTCG GCGTGCGGTC CTCCCTCTCT TGTAGGAGTG TGGGCTTCGT

401 CTTGGCCTCC ACCTCCAGC AGCCCTCACT GCCAGTAAAG TCCAAGTATC ACTCTATGGG AAGTCTGGG ATTGAACAA AATCTGCTAC AAGTCAGGAG  
GAACCGGAGG TGGAGGTCCG TCGGGAGTGA CCGTCATTTT AGGTTTCATAG TGAGATACCC TTCAGGACCC TAAACTTGTT TTAGACGATG TTCAGTCCTC

501 TTCCCTTAT TGAANAATGA ATGATTGAGT GGATGATTGA GAAGCTGTTT CCGTGGGTGA TCCTCACCCC CCTCGACTGC TTCTGGGAGG GAGCCAAACT  
AAGGGGAATA ACTTTTACCT TACTAACTCA CCTACTAACT CTTCGACAAA GGCAGCACT AGGAGTGGG GGAGCTGACG AAGACCTCC CTCGGTTTGA

**FIG. 11A**

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601 CCAAGGGGC TCCGCCTACC TGCCCGGCCG CCCGGATATC CAGTGGACCA ACTGGATCC AGAGCAGCTG CTGGAGGAGC TGGTCCCTT TGCCTCCCTT  
GGTTCCCCCG AGGCGGATGG ACGGCGCGGC GGGCCTATAG GTCACCTGGT TGGACCTAGG TCTCGTCGAC GACCTCCTCG ACCCAGGGAA ACGAGGGAA

701 GAGGGCTTC GGGAGCTGCT AGACAAGGCA CAGGTGGGCC AGGCCTACGT GGGCGGCC TGTCTGCACC CTGATGACCT CCAC TGCCCCA CCTAGTGCCC  
CTCCGAAGG CCCTCGACGA TCTGTTCCGT GTCCACCCCG GTCCAGATGCA CCCCCCGG ACAGACGTGG GACTACTGGA GGTACGGGT GGATCAGGGE

801 CCAACCATCA CAGCAGGCAG GCTCCCAATG TGGCTCAGCA GCTGAGTGG GGTGCCATG GCTTCTCCA CAAATTCATG CACTGGCAGG AGGAATTGCT  
GGTTGGTAGT GTCGTCCGTC CGAGGGTTAC ACCGAGTGCT CGACTCACCC CCGACGSTAC CGAAGAGGT GTTAAAGTAC GTGACCGTCC TCCTTAACGA

901 GCTGGGAGGC ATGGCCAGAG ACCCCCAAGG AGAGCTGCTG AGGCAGAGG CCCTGCAGAG CACCTTCTTG CTGATGAGTC CCCGCCAGCT GTACGAGCAT  
CGACCCTCCG TACCGGTCTC TGGGGTTCC TCTCGACGAC TCCCGTCTCC GGGACGTCTC GTGAAGAAC GACTACTCAG GGGCGGTCCA CATGCTCGTA

1001 TTCCGGGGTG ACTATCAGAC ACATGACATT GGTGGAGTG AGGAGCAGGC CAGCACAGTG CTACAAGCCT GGCAGCGGCG CTTTGTGCAG CTGGCCCCAGG  
AAGGCCCCAC TGATAGTCTG TGTA CTGTAA CCGACCTCAC TCCTCGTCCG GTCGTGTCAC GATGTTCCGA CCGTCGCCG GAAACACGTC GACCGGGTCC

1101 AGGCCCTGCC TGAGAACGCT TCCCAGCAGA TCCATGCTCTT CTCCTCCACC ACCCTGGATA ACATCCTGCA TCGTCTCTCT GAATCAGTG CTGCCCCGTGT  
TCCGGGACGG ACTCTTGCGA AGGTCTGTCT AGGTACGGAA GAGGAGGTGG TGGACCTAT TGTAGGACGT ACGCAAGAGA CTTCACTCAC GACGGGCACA

1201 GGTGGGAGGC TATCTGCTCA TGCTGGCCTA TGCTGTGTG ACCATGCTGC GGTGGGACTG CGCCCAGTCC CAGGGTTCCG TGGGCTTGC CGGGGTACTG  
CCACCCTCCG ATAGACGAGT ACGACCGGAT ACGGACACAC TGGTACGAGC CCACCCTGAC GCGGGTCAGG GTCCCAAGGC ACCCGGAACG GCCCCATGAC

1301 CTGGTGGCCC TGGCGGTGGC CTCAGGCCCTT GGGCTCTGTG CCCTGCTCGG CATCACCTTC AATGCTGCCA CTACCCAGGT GCTGCCCTTC TTGGCTCTGG  
GACCACCGG ACCGCCACCG GAGTCCGGAA CCGGAGACAC GGGACGAGCC GTAGTGAAG TTACGACGT GATGGTCCA CGACGGGAAG AACCGAGACC

FIG. 11B

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1401 GAATCGGCGT GGATGACGTA TTCTGTCTGG CGCATGCCCTT CACAGAGGCT CTGCCTGGCA CCCCTCTCCA GGAGCGCATG GCGAGTGTTC TGCAGCGCAC  
CTTAGCCGCA CCTACTGCAT AAGGACGACC GCGTACGGAA GTGTCTCCGA GACGGACCGT GGGGAGAGGT CCTCGCGTAC CCGTCCACAG ACGTCGCGTG

1501 GGGCACCAGT GTCGTACTCA CATCCATCAA CAACATGGCC GCCTTCCTCA TGGCTGCCCT CGTTCCCATC CCTGCGCTGC GAGCCTTCTC CTTACAGCCA  
CCCCGTGGTCA CAGCATGAGT GTAGGTAGTT GTTGTACCGG CGGAAGGAGT ACCGACGGGA GCAAGGGTAG GGACGCGACG CTCGGAAGAG GAATGTCTGGT

1601 TCCTCAGCCT GGACCTACGG CGGCGCCACT GCCAGGSCCT TGATGTGCTC TGCTGCTTCT CCAGTCCCTG CTCTGCTCAG GTGATTCAGA TCCTGCCCCCA  
AGGAGTCGGA CCTGGATGCC GCCGCGGTGA CCGTCGGGGA ACTACACGAG ACGACGAAGA GGTACGGGAC GAGACGAGTC CACTAAGTCT AGGACGGGGT

1701 GGAGCTGGGG GACGGGACAG TACCAGTGGG CATTGGCCAC CTCACTGCCA CAGTTCAAGC CTTTACCCAC TGTGAAGCCA GCAGCCAGCA TGTGTCAACC  
CCTCGACCCC CTGCCCTGTC ATGGTCACCC GTAACGGGTG GAGTGACGGT GTCAAGTTGG GAATGGGTG AACTTCGGT CGTCGGTCTG ACACCAATGG

1801 ATCTGCTCTC CCCAAGCCCA CCTGGTGCCC CCACCTTCTG ACCCACTGGG CTCTGAGCTC TTCAGCCCTG GAGGGTCCAC ACGGGACCTT CTAGGCCAGG  
TAGGACGGAG GGGTTCGGGT GGACCACGGG GGTGAAGAC TGGGTGACCC GAGACTCGAG AAGTCGGGAC CTCCCAGGTG TGCCCTGGAA GATCCGGTCC

1901 AGGAGGAGAC AAGGCAGAG GCAGCCTGCA AGTCCCTGCC CTGTGCCCGC TGAATCTTG CCCATTTCGC CCGGAATTC CTGCAGCCCG GGGGATCCAC  
TCCTCCTCTG TTCCGTCTTC CGTCGGACGT TCAGGGACGG GACACGGGG ACCTTAGAAC GGGTAAAGCG GGGCCCTTAAG GACGTCTGGG CCCCCTAGGTG

2001 TAGTTCTAGA GCGGCCGCCA CCGCGGTGGA GCTCCAGCTT TTGTTCCCTT TAGTAGGGT TAATTGGCG CTTGGGTATC TT  
ATCAAGATCT CGCCGCGCGT GCGGCCACCT CGAGGTCGAA AACAGGGAA ATCACTCCCA ATTAACGGC GAACCCATAG AA

FIG.-11C

1 GTTATTTCAG GCCATGGTGT TGCGCCGAAT TAATTCCCGA TCCAGACATG ATAAGATACA TTGATGAGTT TGGACAAACC ACAACTAGAA TGCAGTGA  
CAATAAAGTC CGGTACCACA ACGCGGCTTA ATTAAGGCTT AGGTCTGTAC TATTCTATGT AACTACTCAA ACCTGTTTGG TGTTGATCTT ACGTCACCTT

101 AAAATGCTTT ATTGTGAAA TTTGTGATGC TATTGCTTTA TTTGTAACCA TTATAAGCTG CAATAAACAA GTTGGGCCAT GGCGGCCAAG CTTCTGCAGG  
TTTACGAAA TAAACACTTT AAACACTAGC ATAACGAAAT AAACATTGGT AATATTGAC GTTATTGTT CAACCCGGTA CCGCCGGTTC GAAGACGTCC

201 TCGACTCTAG AGGATCCCCG GGGATTTCCG GCATGACTCG ATCGCCGCC ATCAGAGAGC TGCCCGCCGAG TTACACACCC CCAGCTCGAA CCGCAGCACC  
AGCTGAGATC TCCTAGGGG CCCTTAAGGC CGTACTGAGC TAGCGCGGG GAGTCTCTCG ACGGGGCTC AATGTGTGG GGTGAGCTT GCGTCTGTGG

301 CCAGATCCTA GCTGGGAGCC TGAAGGCTCC ACTCTGGCTT CGTCTTACT TCCAGGGCCT GCTCTTCTCT CTGGGATGCG GGATCCAGAG ACATTGTGGC  
GGTCTAGGAT CGACCTCTCG ACTTCCGAGG TGAGACCGAA GCACGAATGA AGGTCCCGGA CGAGAAGAGA GACCTACGC CCTAGGTCTC TGTAACACCG

401 AAAGTGCTCT TTCTGGGACT GTTGGCCTTT GGGCCCTTGG CATTAGGTCT CCGCATGGCC ATTATTGAGA CAAACTTGA ACAGCTCTGG GTAGAAGTGG  
TTTCACGAGA AAGACCTTGA CAACCGGAAA CCGCGGAGC GATATCCAGA GCGTACCGG TAATAACTCT GTTGAACCT TGTCGAGACC CATCTTCACC

501 GCAGCCGGGT GAGCCAGGAG CTGCATTACA CCAAGGAGAA GCTGGGGGAG GAGGTGCGAT ACACCTCTCA GATGCTGATA CAGACCGCAC GCCAGGAGGG  
CGTCGGCCCA CTCGGTCTCT GACGTAATGT GTTCTCTCTT CGACCCCTCT CACCGAGCTA TGTGGAGAGT CTACGACTAT GTCTGGCGTG CCGTCTCTCC

601 AGAGAACATC CTCACACCCG AAGCATTGCG CCTCCACCTC CAGCAGCCCC TCACTGCGAG TAAAGTCCAA GTATCACTCT ATGGGAAGTC CTGGGATTGG  
TCTCTTGTAG GAGTGTGGC TTCTGTGACC GAGGTGGAG GTCCGTGGG AGTGACGCTC AGTGCAGCTT ATTCAGGTT CATAGTGAGA TACCCTTCAG GACCTAAAC

701 AACAAAATCT GCTACAAAGTC AGGAGTTCCC CTTATTGAAA ATGGAATGAT TGAGTGGATG ATTGAGAAGC TGTTTCCGTG CGTGATCTC ACCCCCTCG  
TTGTTTGTAG CGATGTTTAC TCCTCAAGG GAATAACTTT TACCTTACTA ACTCACTTAC TAACCTCTCG ACAAAGGCAC GCACTAGGAG TGGGGGAGC

801 ACTGCTTCTG GAGGGAGGCC AAACCTCCAG GGGCTCCG CTACTGCCC GCGCGCCCG ATATCCAGTG GACCAACCTG GATCCAGAGC AGCTGCTGGA  
TGACGAAGAC CTTCCCTCTG TTTGAGGTTT CCGGAGGCG GATGACGCGG CCGGGGCGG TATAGTTCAC CTGTTGGAC CTAGGTCTCG TCGACGACCT

91 S R V S Q E L H Y T K E K L G E E A A Y T S Q M L I Q T A R Q E G

124 E N I L T P E A L G L H L Q A A L T A S K V Q V S L Y G K S W D L

157 N K I C Y K S G V P L I E N G M I E W M I E K L F P C V I L T P L D

191 C F W E G A K L Q G G S A Y L P G R P D I Q W T N L D P E Q L L E

FIG. 1A

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901 GGAGCTGGGT CCCTTGGCT CCCTGAGG CTTCCGGGAG CTGCTAGACA AGGCACAGGT GGGCCAGGCC TAGCTGGGGC GGCCCTGTCT GCACCCTGAT  
 CCTCGACCCA GGGAAACGGA GGGAACTCCC GAAGGCCCTC GAGGATCTGT TCCGTGTCCA CCGGTGCCG ATGACCCCG CCGGACAGA CGTGGGACTA  
 224 E L G P F A S L E G F R E L L D K A Q V G Q A Y V G R P C L H P D  
 1001 GACCTCCACT GCCCACCTAG TGCCCCAAC CATCACAGCA GGCAGGCTCC CAATGTGGCT CACGAGCTGA GTGGGGCTG CCATGGCTTC TCCCACAAAT  
 CTGGAGGTGA CCGGTGGATC ACGGGGTTG GTAGTGTCTG CCGTCCGAGG GTTACACCGA GTGCTCGACT CACCCCCGAC GGTACCGAAG AGGTGTTTA  
 257 D L H C P P S A P N H H S R Q A P N V A H E L S G G C H G F S H K F  
 1101 TCATGCACTG GCAGGAGGAA TTGCTGCTGG GAGGCATGGC CAGACACCCC CAAGGACAGC TGCTGAGGGC AGAGGCCCTG CAGAGCACCT TCTTGCTGAT  
 AGTACGTGAC CGTCTCTCTT AACGACGACC CTCCTGTACC GTCTCTCTCG ACCTCTCCG TCTCCGGGAC GTCTCGTGA AGAACGACTA  
 291 M H W Q E E L L L G G M A R D P Q G E L L R A E A L Q S T F L L M  
 1201 GAGTCCCCGC CAGCTGTACG AGCATTTCCG GGGTACTAT CAGACACATG ACATTGGCTG GAGTGAGGAG CAGGCACGCA CAGTGCTACA AGCCTGGCAG  
 CTCAGGGCG GTCCACATGC TCGTAAAGGC CCCACTGATA GTCTGTGTAC TGTAAACGAC CTCACTCCTC GTCCGTCTG GTCACGATGT TCGGACCGTC  
 324 S P R Q L Y E H F R G D Y Q T H D I G W S E E Q A S T V L Q A W Q  
 1301 CGCGCGTTTG TGCAGCTGCC CCAGGAGGCC CTGCCTGAGA ACGCTTCCCA GCAGATCCAT GCCTTCTCCT CCACCACCTT GGATGACATC CTGCATGCGT  
 GCGCGAAAC ACGTCACCG GGTCTCCCG GACCGACTCT TCGGAAGGT CGTCTAGGTA CGGAAGAGGA GTGTGTGGGA CCTACTGTAG GACGTACGCA  
 357 R R F V Q L A Q E A L P E N A S Q Q I H A F S S T T L D D I L H A F  
 1401 TCTCTGAAGT CAGTGTGCC CGTGTGGTGG GAGGTATCT GCTCATGTGT GCCTATGCC CTGTGACCAT GTGTGGTGG GACTGGCCCC AGTCCCAGGG  
 AGAGACTTCA GTCACGACCG GCACACCACC CTCGATAGA CGAGTACGAC CGGATACGGA CACACTGGTA CGACGCCACC CTGACGCGG TCAGGGTCCC  
 391 S E V S A A R V V G G Y L L M L A Y A C V T M L R W D C A Q S Q G  
 1501 TTCCGTGGGC CTTGCCGGG TACTGCTGGT GGCCCTGGCG GTGGCCTCAG GCCTTGGGCT CTGTGCCCTG CTCGGCATCA CCTTCAATGC TGCCACTACC  
 AAGGCACCG GAACGGCCC ATGACGACCA CCGGACCGC CACCGAGTC CGGAACCCGA GACACGGGAC GAGCCGTAGT GGAAGTTACG ACGGTGATGG  
 424 S V G L A G V L L V A L A V A S G L G L C A L L G I T F N A A T T  
 1601 CAGGTGCTGC CTTTCTTGGC TCTGGGAATC GCGGTGGATG ACGTATTCT GCTGGCGCAT GCCTTCACAG AGGCTCTGCC TGGCACCCCT CTCCAGGAGC  
 GTCCACGACG GAAAGAACCG AGACCCTTAG CCGCACTTAC TGCATAAGGA CGACCGGTA CGGAAGTGT TCCGAGACCG ACCGTGGGA GAGGTCTTCG  
 457 Q V L P F L A L G I G V D D V F L L A H A F T E A L P G T P L Q E R  
 1701 GCATGGGCGA GTGTCTGCAG CGCACGGGCA CCAGTGTCTG ACTCACATCC ATCAACAACA TGGCCGCCTT CCTCATGGCT GCCCTCGTTC CCATCCCTGC  
 CGTACCCGCT CACAGACGTC GCGTGCCCGT GGTACAGCA TGAGTGTAGG TAGTTGTTGT ACCGGCGGAA GGAGTACCGA CCGGAGCAAG GGTAGGAGC  
 491 M G E C L Q R T G T S V V L T S I N N M A A F L M A A L V P I P A

FIG. 1B

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2701 GCTCATCCAG ACTGAGACG CCCAGGAGCC TCTGGATTTC AGCCAGCTGA CCACAAGGAA GCTGGTGGAC AGAGAGGGAC TGATTCCACC CGAGCTCTTC  
CGAGTAGGTC TGACCTCTGC GGTCTCTCGG AGACCTAAG TCGGTGCACT GGTGTTCTTT CGACCACCTG TCTCTCCCTG ACTAAGGTGG GCTCGAGAAG  
824 L I Q T G D A Q E P L D F S Q L T T R K L V D R E G L I P P E L F  
2801 TACATGGGC TGACCGTGTG GGTGAGCAGT GACCCCTCTGG GTCTGGCAGC CTCACAGGCC AACTTCTACC CCCACCTCC TGAATGGCTG CACGACAAAT  
ATGTACCCCG ACTGGCACAC CCACTCGTCA CTGGGGGACC CAGACCGTGG GAGTGTCCGG TTGAAGATGG GGGGTGGAGG ACTTACCGAC GTGCTGTTTA  
857 Y M G L T V W V S S D P L G L A A S Q A N F Y P P P P E W L H D K Y  
2901 ACGACACCAC GGGGGAGAAC CTTCCGATCC CGCAGCTCA GCGCTTGGAG TTGCCCCAGT TCCCTTCTCT GCTGCGTGGC CTCAGAAGA CTGCAGACTT  
TGCTGTGGTG CCCCCTCTTG GAAGCGTAGG GCGGTCTAGT CCGGAACCTC AAACGGGTCA AGGGAAGGA CGACGCACCG GAGGTCTTCT GACGTCTGAA  
891 D T T G E N L R I P P A Q P L E F A Q F P F L L R G L Q K T A D F  
3001 TGTGAGGCC ATCGAGGGG CCGGGCAGC ATGGCAGAG GCGGGCCAG CTGGGGTGCA CGCTACCCC AGCGGCTCCC CCTTCTCTCT CTGGGAACAG  
ACACCTCCG TAGCTCCCC GGGCCCGTCG TACGCTCTC CCGCCGCTCC GACCCACGT CGGATGGGG TCGCCGAGGG GGAAGGAGAA GACCCCTGTC  
924 V E A I E G A R A A C A E A G Q A G V H A Y P S G S P F L F W E Q  
3101 TATCTGGGC TGCGCGCTG CTTCTCTGTC GCGCTCTGCA TCCTGCTGGT GTGCACTTTC CTCTGCTGTG CTCTAACCCC TGGACGGCTG  
ATAGACCCG ACGCCGCGAC GAAGACGAC CGGCAGACGT AGGACGACCA CACGTGAAG GAGCAGACAC GAGACGACGA GGAGTGGGG ACCTGCCGAC  
957 Y L G L R R C F L L A V C I L L V C T F L V C A L L L L N P W T A G  
3201 GCCTCATAGT GCTGGTCCTG GCGATGATGA CAGTGGAACT CTTTGGTATC ATGGGTTTCC TGGGCATCAA GCTGAGTGCC ATCCCCGTGG TGATCCTTGT  
CGGAGTATCA CGACCAGGAC CGCTACTACT GTCACCTTGA GAAACCATAG TACCCAAAGG ACCCGTAGTT CGACTCACGG TAGGGGCACC ACTAGGAACA  
991 L I V L V L A M M T V E L F G I M G F L G I K L S A I P V V I L V  
3301 GGCTCTCTGA GGCATTGGCG TTGAGTTTAC AGTCCACCTG GGTCTGGGCT TCCTGACCCAC CCAGGGCAGC CGGAACCTGC GGGCCGCCCA TGCCCTTGAG  
CCGGAGACAT CCGTAACCGC AACTCAAGT TCAGGTGCAC CGAGACCCGA AGGACTGGTG GGTCCCGTGG CCCTTGGACG CCCGGCGGGT ACGGAACTC  
1024 A S V G I G V E F T V H V A L G F L T T Q G S R N L R A A H A L E  
3401 CACACATTG CCCCCGTGAC CGATGGGGC ATCTCCACAT TCCTGGGTCT GCTCATGCTT GCTGGTTCCC ACTTTGACTT CATTGTAAGG TACTTCTTTG  
GTGTGTAAC GGGGGCACTG GCTACCCCGG TAGAGGTGTA ACCACCCAGA CGAGTACGAA CGACCAAGGG TGAACCTGAA GTAACATCC ATGAAGAAAC  
1057 H T F A P V T D G A I S T L L G L L M L A G S H F D F I V R Y F F A  
3501 CGCGCTGAC AGTCTCACG CTCCTGGGCC TCCTCCATGG ACTCTGCTG CTGCTGTGCT TGCTGTCCAT CCTGGGCCCC CGGCCAGAGG TGATACAGAT  
GCCGCGACTG TCACGAGTGC GAGGACCCCG AGGAGGTACC TGAGCAGCAG CACGACGAC GACGACGTA GACCCCGGGC GCGGCTCTCC ACTATGTCTA  
1091 A L T V L T L L G L L H G L V L L P V L L S I L G P P P E V I Q M

FIG. 1D

$\frac{4}{27}$   
1146

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3501 GTACAAGGAA AGCCAGAGA TCCTGAGTCC ACCAGTCCA CAGGAGGCG GGCTTAGGTG GGGGCATCG TCCTCCCTGC CCCAGAGCTT TGCCAGAGTG  
 CATGTTCCCTT TCGGGTCTCT AGGACTCAGG TGGTCGAGGT GTCCCTCCGC CCGAATCCAC CCCCGTAGG AGAGGGACG GGGTCTCGAA ACGTCTCAC  
 1124 Y K E S P E I L S P P A P Q G G G L R W G A S S S L P Q S F A R V  
 3701 ACTACCTCCA TGACCGTGGC CATCCACCCA CCCCCCTGC CTGGTGCCCTA CATCCATCCA GCCCCCTGATG AGCCCCCTTG GTCCCTTGCT GCCACTAGCT  
 TGATGGAGGT ACTGGCACCG GTAGGTGGGT GGGGGGACG GACCACGGAT GTAGGTAGGT CGGGGACTAC TCGGGGGAAC CAGGGACGA CCGTGATCGA  
 1157 T T S M T V A I H P P P L P G A Y I H P A P D E P P W S P A A T S S  
 3801 CTGGCAACCT CAGTTCAGG GGACCAAGTC CAGCCACTGG GTGAAAGAGC AGCTGAAGCA CAGAGACCAT GTGTGGGCG TGTGGGTCA CTGGGAAGCA  
 GACCGTTGGA GTCAAGGTCC CCGGTCCAG GTCGGTGACC CACTTCTCG TCGACTTCGT GTCTCTGGTA CACACCCCG ACACCCAGT GACCCCTCGT  
 1191 G N L S S R G P G P A T G O  
 3901 CTGGGTCTGG TGTAGACGC AGGACGGACC CCTGGAGGGC CTGCTGCTG CTGCAATCCC TCTCCGACC CAGCTGTCTAT GGGCCTCCCT GATATCGAAT  
 GACCCAGACC ACAATCTGCG TCCTGCCTGG GGACCTCCCG GGACGACGAC GACGTAGGGG AGAGGGCTGG GTCGACAGTA CCCGGAGGGA CTATAGCTTA  
~~ATTC (silent)~~  
~~PKT follows, this is the 5' prime end of vector~~

4001 TCAATCGATA GAACGAGGT GCAGTTGGAC  
 AGTAGCTAT CTTGGCTCCA CGTCAACCTG

FIG. 1E

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~~(SEQ ID NO: 3)~~ e

	30	40	50	60	70
905531	GCTGGGGTGACGCCTACCNCAGCGGNTCCCCCTTCCTCTTCTGGGAACA				
	::: :: : *****				
hpatched	CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCA				
<del>(SEQ ID NO: 4)</del> e	3010	3020	3030	3040	3050

	80	90	100	110	120
905531	GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGCTGCATCCTGCTGG				
	*** * ***** *				
hpatched	GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTTCATCAGCGTGGTGTG				
	3060	3070	3080	3090	3100

	130	140	150	160	170
905531	TGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTNAACCCCTGGACGGCT				
	*****				
hpatched	CCTGCACATTTCCTCGTGTGCGCTGTCTTCCTTCTGAACCCCTGGACGGCC				
	3110	3120	3130	3140	3150

	180	190	200	210	220
905531	GGCCTNATAGTGCTGGTCCTGGCGATGATGACAGTGGAACTCTTTGGTAT				
	** *****				
hpatched	GGGATCATTTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTGTTTCGGCAT				
	3160	3170	3180	3190	3200

	230	240	250
905531	CATGGGTTTNCCTGGGCATCAAGCTGAGT		
	*****		
hpatched	GATGGGCCTCATCGGAATCAAGCTCAGT		
	3210	3220	3230

	80	90	100	110	120
905531	TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGCTGCATCCTGCTGGTGT				
	::: ::: *				
hpatched	GCTGCTGCTGTTTCATCAGCGTGGTGTGGCC---TGCACATTTCCTCGTGT				
	3090	3100	3110	3120	

	130	140	150
905531	GCACTTTCCTCGTCTGTGCTCTGCTGCT		
	* *		
hpatched	GCGCTGTCTTCCTTCTGAACCCCTGGAC		
	3130	3140	3150

FIG. 2A

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(SEQ ID NO: 5) 1326258 30 40 50 60 70  
GCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGAACA  
::: :: : \*\*\*\*\*  
hpatched CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGAGCA  
3010 3020 3030 3040 3050

1326258 80 90 100 110 120  
GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGG  
\*\*\* \* \*\*\*\*\* \* \* \* \* \*  
hpatched GTACATCGGCCTCCGCCACTGGCTGCTGCTTCATCAGCGTGGTGTGG  
3060 3070 3080 3090 3100

1326258 130 140 150  
TGTGCACTTTCCTCNTCTGTGCTCT  
\*\*\*\*\*  
hpatched CCTGCACATTCTCGTGTGCGCTGT  
3110 3120 3130

1326258 90 100 110 120 130  
TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGT  
::: ::: \* \* \* \* \*  
hpatched GCTGCTGCTGTTTCATCAGCGTGGTGTGGCC---TGCACATTCTCGTGT  
3090 3100 3110 3120

1326258 140 150  
GCACTTTCCTCNTCTGTGCTCT  
\*\* \* \* \* \*  
hpatched GCGCTGTCTTCCTTCTGAACCC  
3130 3140

1326258 10 20 30 40 50  
CCGGGCAGCATGCGCAGAGGCCGCGCCAGGCTGGGGTGCACGCCTACCCCA  
\*\*\*\*\*  
(SEQ ID NO: 6) hpatched.RC CCGGGCGGCATG--CGGAAGCGGACCACGCTGGGGGGTGGCTCAGGGGAG  
710 720 730 740 750

FIG. 2B

(SEQ ID NO: 1)  
(SEQ ID NO: 2)

1 MASAGNAEPODRGGGSGCIGAPRPAGGGRRRTGGLRRAAAPDRDYL  
1 .....MTRSPPLREL

PTCH  
PTCH2

51 HRPSYCDAAFALEQISKGKAATGRKAPLWLRAKFQRLLFKLGCIQKNCCK  
11 .PPSYTPP..ARTAAPQILAGSLKAPLWLRAYEQGLLES LGCGIQRHCGK

PTCH  
PTCH2

101 FLVVGLLFCGAFVGLKAAANL ETNVEELWVEVGGRVSRRELNYTRQKIGEE  
58 VLEFLGLLAFGALLALGLRMAI IETNLEQLWVEVGSRVSRQELHYTKEKLGEE

TM1

PTCH  
PTCH2

151 AMFNPPQLMTQTTPKEEGANVLTTEALLQHLD SALLQASRVHVYMYNRRQMKLE  
108 AAYTSQMLIQTARQEGENILTP EALGLHLQAALTASKVQVSLY GKSWDLN

PTCH  
PTCH2

201 HLCYKSGGELITEITGYMDQII EYLYPCLTITPLDCFWEGAKLQSGTAYLLG  
158 KICYKSGGVPLIENGMI EWMI EKLFP CVILTP LDCFWEGAKLQSGSAYLP

PTCH  
PTCH2

251 KPPLRWTFDPLEFLEELKKIN YQVDSWEMLNKAEVGHVGHYMDRPCLNPA  
208 RPDIQWTLNLDPEQLLEELGPFA.SLEGFRELLDKAQVQA VVGRRPCLHDP

PTCH  
PTCH2

301 DPDCPATAPNKNSTKPLDMALV L NGGCHGLSRKYIMHWQEELIVGGTVKNS  
257 DLHCPPSAPNHH SRQAPNVIAHEL SGGCHGFSHKFFIMHWQEELLLGGMARDP

PTCH  
PTCH2

351 TGKLVSAHALQTMFQLMTPKQMYEHFKGYEVVSH .INWNEDKAAAILLEAW  
307 QGELLRAEALQSTFLLMSPRQLYEHFRG.DYQTHDJGWSEEQASTVLCQAW

PTCH  
PTCH2

400 QRTYVEVVHQSVAQNSTQKVLSTTTTTLDDILKSFSDVSVRVASGYLLM  
356 QRRFVQLAQEALPENASQQIHAFSS T T L D D I L H A F S E V S A A R V V G G Y L L M

TM2

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FIG. 3A

# TM3

PTCH 450 L A Y A C L T M L R W D C S K S Q G A V G L A G V L L V A L S V A A G L G L C S L I G S F N A A T  
PTCH2 406 L A Y A C V T M L R W D C A Q S O G S V G L A G V L L V A L A V A S G L G L C A L L G T F N A A T

# TM4

PTCH 500 T Q V L P F L A L G V G V D D V E L L A H A F S E T G Q N K R I P F E D R T G E C L K R T G A S V A A  
PTCH2 456 T Q V L P F L A L G V G V D D V E L L A H A F T E A L P G . . T P L O E R M G E C L Q R T G T S V V

# TM5

PTCH 550 L T S I S N V T A F F M A A L I P I P A L R A F S L Q A A V V V F N F A M V L L I F P A L S M D  
PTCH2 504 L T S I N N M A A F L M A A L V P I P A L R A F S L Q A A V V G C T E V A V M L V F P A L L S L D

# TM6

PTCH 600 L Y R R E D R R L D I F C C F T S P C V S R V I Q V E P Q A Y T D T H D N T R Y S P P P P Y S S H S  
PTCH2 554 L R R R H C Q R L D V L C C F S S P C S A Q V I Q I L P O E L G D G T . . . . . V P V G

PTCH 650 F A H E T Q I T M Q S T V Q L R T E Y D P H T H V Y T T A E P R S E I S V Q P V T V T Q D T L S C  
PTCH2 593 I A H . . . . . L T A T V Q A F T H C E A S S Q H V V I I L P P Q A H L V P P P . . . . . S D P L L G S

PTCH 700 Q S P E S T S T R D L L S Q F S D S S L H . . C L E P P C T K W T L S S F A E K H Y A P F L L K P  
PTCH2 634 E L F S P G G S T R D L L G Q E E E T R Q K A A C K S L P C A R W N L A H F A R Y Q F A P L L L Q S

# TM7

PTCH 748 K A K V V I F L F L G L L G V S L Y G T T R V R D G L D L T D I V P R E T R E Y D F I A A Q F K Y  
PTCH2 684 H A K A V L V L F G A L L G L S L Y G A T L V Q D G L A L T D V V P R G T K E H A F L S A Q L R Y

PTCH 798 F S F Y N M Y I V T Q K A . D Y P N I Q H L L Y D L H R S F S N V K Y V M L E E N K Q L P K M W L H  
PTCH2 734 F S L Y E V A L V T Q G G F D Y A H S Q R A L F D L H Q R F S S L K A V L P P P A T Q A P R T W L H

FIG. 3B

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PTCH 847 YFRDWLQGLQDAFDSWETGKTI MPNNYKNGSDDGVLAYKLLVQTGSRDKP  
 PTCH2 784 YYRNWLQGIQAADFQDQWASGRJITRHSYRNGSE DGA LAYKLLIQTGDAQEP

\*\*\*

PTCH 897 IDISQLTKQRLVDADGIIINPSAFYIYLTAWVSNDPVA YAASQANIRPHRP  
 PTCH2 834 LDFSQLTTRKLLVDREGLLJPPELFYMG LITVWVSSDPLGLAASQANFYPPPP

PTCH 947 EWVHDKADYMPETRLRIPAAEPIEYAOFPFYLNGLRDTSDFVEAIEKVRT  
 PTCH2 884 EWLHDKYD.TTGENLRIPPAQPLEEFAOFPFLLRGLQKTA DFVEAIEGAR A

TM8

PTCH 997 ICSNYTSLGLSSYPNGYYPFLFWEQYI GLRHWL LLLFISVVLA CTFLVCAVF  
 PTCH2 933 ACIAEAGQAGVHAYPSGSPFLFWEQYI GLRRCFLLAVCILLVCTFLVCA L

TM9

PTCH 1047 L LNPWTAGITVMVLA LMTVELFGMMGLI GIKLSA VPPVILLASVGI GVEF  
 PTCH2 983 L LNPWTAGLIVLVA LMTVELFGIMGFL GIKLSA IIPVVILV ASVGI GVEF

TM10

TM11

PTCH 1097 TVHVALAFLT AIGDKNRRRAVLALAHMFA PVLDGA VSTLLGV LMLAGSEFD  
 PTCH2 1033 TVHVALGFLT TOGSRNLRRAHALEHTFA PVTDGAISTLLGL LMLAGSHFD

TM12

PTCH 1147 FIVRYFFA VLA LTL LGV LNLGLVLLPVLLS FFGPIYPEV SPANGLNRLPTP  
 PTCH2 1083 FIVRYFFA ALTV LTL LGV LNLGLVLLPVLLS ILGPPPEV IQMYKESPEILS

PTCH 1197 SP EPPPSVVR FAMP PGH THSGSDSSDSEYSSOTT VSG LSEELRH YEAOQG  
 PTCH2 1133 PPAP QGGGLRWGASSSL PQS.FARVTTSM TVAIHPPPLPGAYIHPAPDEP

FIG. 3C

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PTCH 1247 AGGPAHQVIVEATENPVFAHSTVVHPESRRHPPSNPRQQPHLDSGSLPPG  
PTCH2 1182 PWSPAATSSGNLSSRGPGPATG  
PTCH 1297 RQQQPRRDPREGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARS  
PTCH 1347 HNPRNPASTAMGSSVPGYCQPIITTTASASVTAVHPPPPVPGGPRNPRGG  
PTCH 1397 LCPGYPETDHGLFEDPHVPFHVRCERRRDSKVEVIELQDVECEERPRGSSS  
PTCH 1447 N

FIG. 3D

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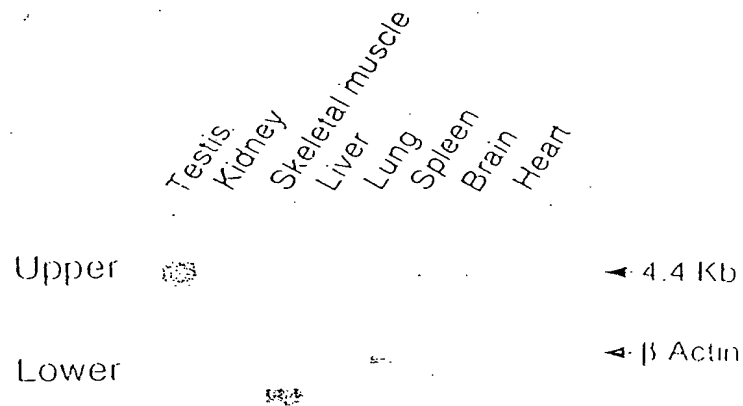


FIG. 4

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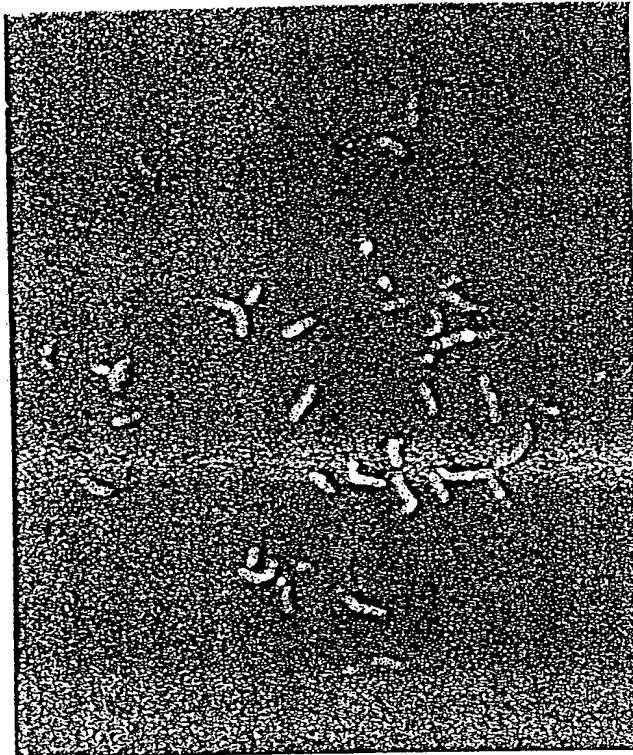


FIG. 5

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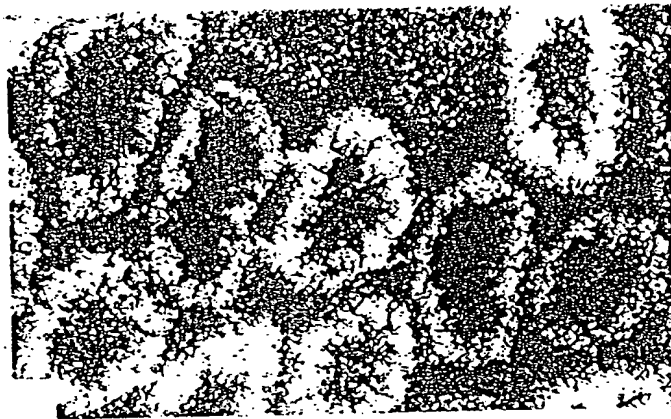


FIG. 6C

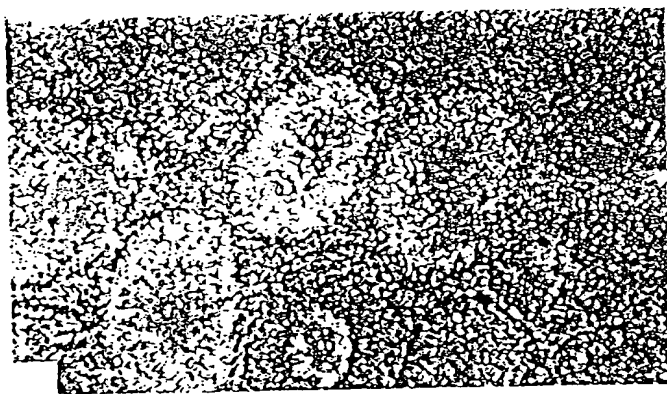


FIG. 6B

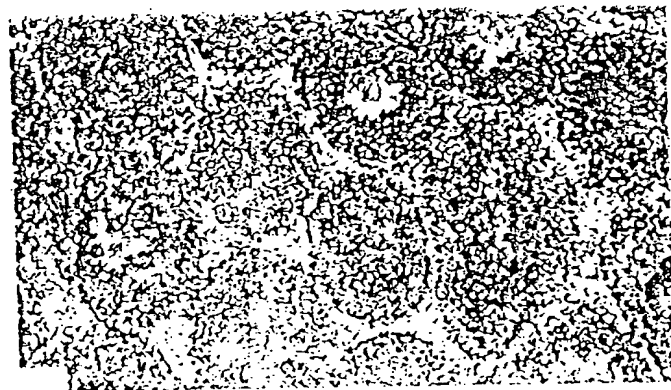


FIG. 6A

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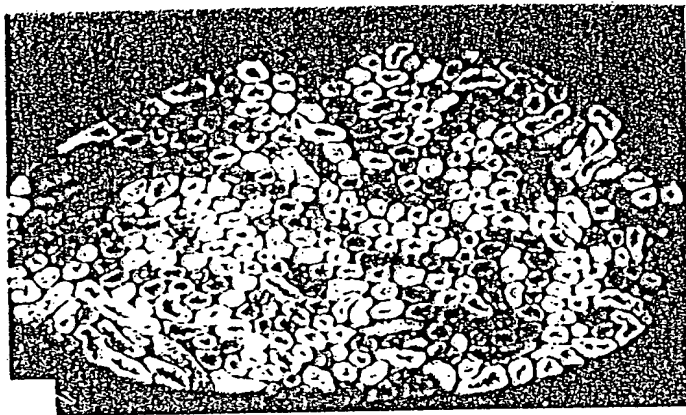


FIG. 6F

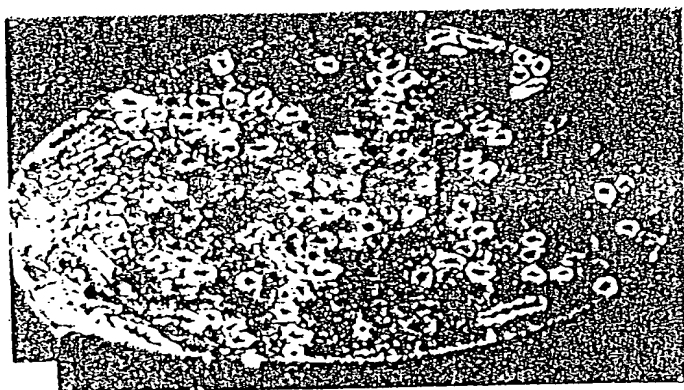


FIG. 6E

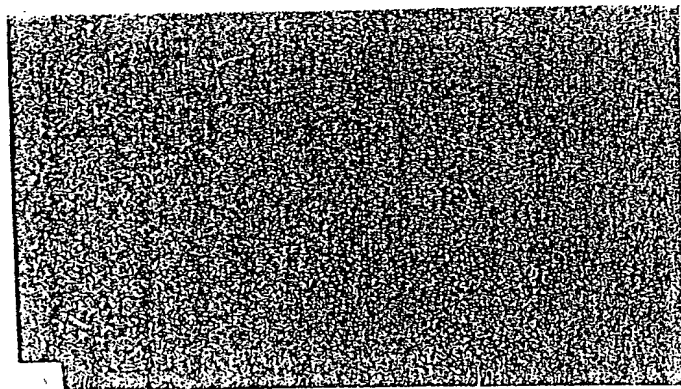


FIG. 6D

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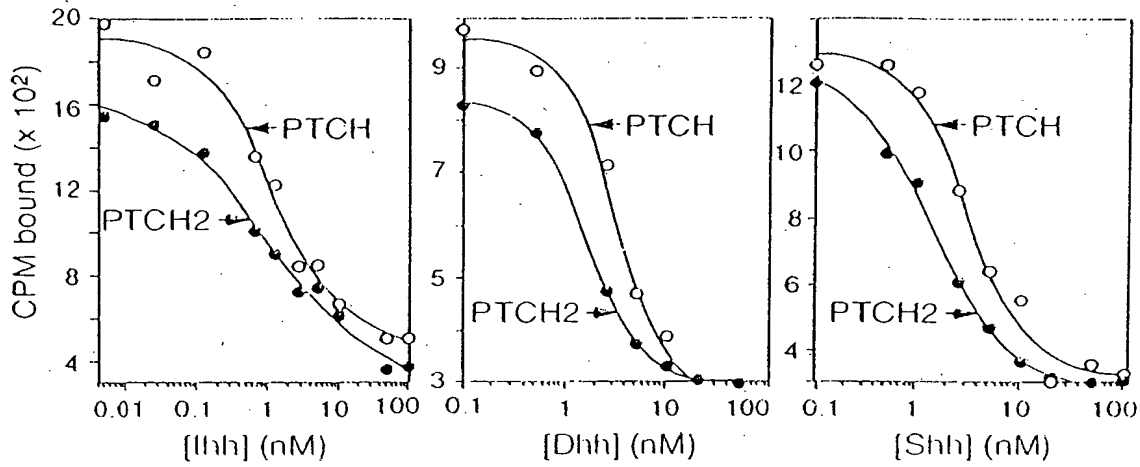


FIG. 7A

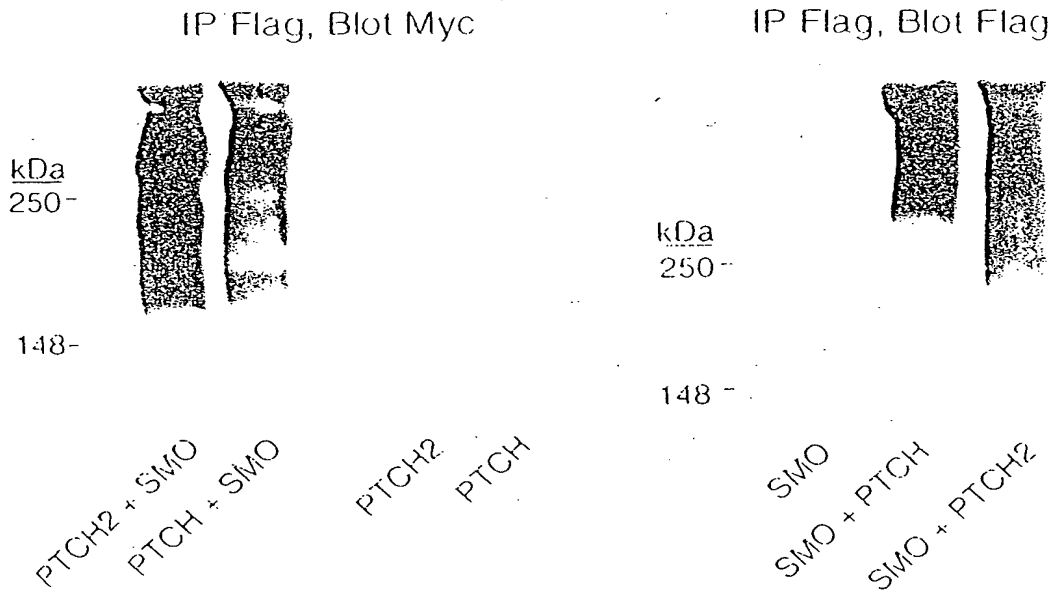


FIG. 7B

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	10	20	30	40	50
<i>hPtch-2</i>	MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCG				
	* * * * *				
<i>mPatched2</i>	MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCR				
<del>(SEQ ID NO: 7)</del>	10	20	30	40	50
	60	70	80	90	100
<i>hPtch-2</i>	IQRHCGKVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYT				
	* * * * *				
<i>mPatched2</i>	IQKHCGKVLFLGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYT				
	60	70	80	90	100
	110	120	130	140	150
<i>hPtch-2</i>	KEKLGEEAAYTSQMLIQATARQEGENILTPEALGLHLQAALTASKVQVSLY				
	* * * * *				
<i>mPatched2</i>	KEKLGEEAAYTSQMLIQTAHQEGGNVLTPEALDLHLQAALTASKVQVSLY				
	110	120	130	140	150
	160	170	180	190	200
<i>hPtch-2</i>	GKSWDLNKICYKSGVPLIENGMIWMIIEKLFPCVILTPLDLDCFWEGAKLQG				
	* * * * *				
<i>mPatched2</i>	GKSWDLNKICYKSGVPLIENGMIERMIEKLFPCVILTPLDLDCFWEGAKLQG				
	160	170	180	190	200
	210	220	230	240	250
<i>hPtch-2</i>	GSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELDDKAQVGQAYVGR				
	* * * * *				
<i>mPatched2</i>	GSAYLPGRPDIQWTNLDPPQQLLEELGPFASLEGFRELDDKAQVGQAYVGR				
	210	220	230	240	250
	260	270	280	290	300
<i>hPtch-2</i>	PCLHPDDLHCPPSAPNHHSRQAPNVAHELSSGGCHGFSHKFMHWQEELLLG				
	* * * * *				
<i>mPatched2</i>	PCLDPDDPHCPPSAPNRHSRQAPNVAQELSSGGCHGFSHKFMHWQEELLLG				
	260	270	280	290	300
	310	320	330	340	350
<i>hPtch-2</i>	GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQAST				
	* * * * *				
<i>mPatched2</i>	GTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASM				
	310	320	330	340	350

FIG. 8A

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	360	370	380	390	400
<i>hPtc-2</i>	VLQAWQRRFVQLAQEALPENASQQIHAFSSTLDDILHAFSEVSAARVVG				
	*****				
<i>mPatched2</i>	VLQAWQRRFVQLAQEALPANASQQIHAFSSTLDDILRAFSEVSTTRVVG				
	360	370	380	390	400
<i>hPtc-2</i>	410	420	430	440	450
	GYLLMLAYACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGIT				
	*****				
<i>mPatched2</i>	GYLLMLAYACVTMLRWDCAQSGAVGLAGVLLVALAVASGLGLCALLGIT				
	410	420	430	440	450
<i>hPtc-2</i>	460	470	480	490	500
	FNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGT				
	*****				
<i>mPatched2</i>	FNAATTQVLPFLALGIGVDDIFLLAHAF TKAPDTP LPERMGECLRSTGT				
	460	470	480	490	500
<i>hPtc-2</i>	510	520	530	540	550
	SVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAIL				
	** *** ** *****				
<i>mPatched2</i>	SVALTSVNNMVAF FMAALVPIPALRAFSLQAAIVVGCNFAAVMLVFPAIL				
	510	520	530	540	550
<i>hPtc-2</i>	560	570	580	590	600
	SLDLRRRHRCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV				
	*****				
<i>mPatched2</i>	SLDLRRRHRCQRLDVLCCFSSPCSAQVIQMLPQELGDRAVPVGIAHLTATV				
	560	570	580	590	600
<i>hPtc-2</i>	610	620	630	640	650
	QAFTHCEASSQHVV TILPPQAH LVPPSDPLGSELFSPGGSTRDLLGQEE				
	*****				
<i>mPatched2</i>	QAFTHCEASSQHVV TILPPQAH LLSPASDPLGSELYSPGGSTRDLLSQEE				
	610	620	630	640	650
<i>hPtc-2</i>	660	670	680	690	700
	ETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLF GALLGLS				
	* *** * ** * *****				
<i>mPatched2</i>	GTGPQAACRPLLCAHWTLAHFARYQFAPLLLQTRAKALVLLFF GALLGLS				
	660	670	680	690	700

FIG. 8B

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	710	720	730	740	750
<i>hPtc-2</i>	LYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYA				
	*****				
mPatched2	LYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYA				
	710	720	730	740	750

	760	770	780	790	800
<i>hPtc-2</i>	HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDW				
	*****				
mPatched2	HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRSWLQGIQAAFDQDW				
	760	770	780	790	800

	810	820	830	840	850
<i>hPtc-2</i>	ASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLV DREGL				
	*****				
mPatched2	ASGRITRHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLTTRKLV DKEGL				
	810	820	830	840	850

	860	870	880	890	900
<i>hPtc-2</i>	IPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP				
	*****				
mPatched2	IPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP				
	860	870	880	890	900

	910	920	930	940	950
<i>hPtc-2</i>	PAQPLEFAQFPFLRLGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSP				
	*****				
mPatched2	AAQPLEFAQFPFLRHGLQKTADFVEAIEGARAACTEAGQAGVHAYPSGSP				
	910	920	930	940	950

	960	970	980	990	1000
<i>hPtc-2</i>	FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMT				
	*****				
mPatched2	FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLSPWTAGLIVLVLAMMT				
	960	970	980	990	1000

	1010	1020	1030	1040	1050
<i>hPtc-2</i>	VELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLT TQGSRNLR				
	*****				
mPatched2	VELFGIMGFLGIKLSAIPVVILVASIGIGVEFTVHVALGFLT SHGSRNLR				
	1010	1020	1030	1040	1050

FIG. 8C

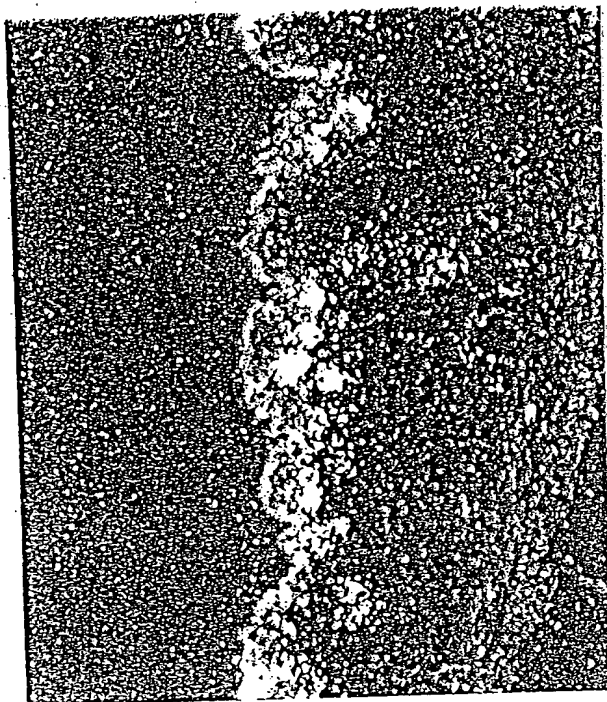
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	1060	1070	1080	1090	1100
<i>hPtch-2</i>	AAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLGL				
	** ***.*****.*****.*****.*****.*****				
<i>mPatched2</i>	AASALEQTFAPVTDGAVSTLLGLLMLAGSNFDFIIRYFFVVLTVLTLGL				
	1060	1070	1080	1090	1100
	1110	1120	1130	1140	1150
<i>hPtch-2</i>	LHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGGLRWGASSSLP				
	****.*****.*.*.*****.*...***.*****.***				
<i>mPatched2</i>	LHGLLLLPVLLSILGPPPQVVQVYKESPQTLNSAAPQRGGLRWDRPPTLP				
	1110	1120	1130	1140	1150
	1160	1170	1180	1190	1200
<i>hPtch-2</i>	QSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP				
	*****.*****.***.***				
<i>mPatched2</i>	QSFARVTTSMTVALHPPPLPGAYVHPASEEPT				
	1160	1170	1180		
<i>hPtch-2</i>	ATG				

FIG. 8D

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PTCH2



PTCH



FIG. 9

~~Consensus sequence of human patched-2 cDNA clone~~  
~~length: 1004 bp~~

(SEQ ID NO: 8)

1 CCCACCGTC CGGAGAAGC TGGGGAGGA GGTGCATAC ACCTCTCAGA TGCTGATACA GACCGCAGC CAGGAGGGAG AGAACATCCT CACACCGGAA  
GGGTGGCAG GCCCTCTTCG ACCCCCTCCT CCGACGTATG TGGAGAGTCT ACGACTATGT CTGGCGTGC GTCTCCCTC TCTGTAGGA GTGTGGGCTT

101 GCACTTGGCC TCCACCTCCA GGCAGCCCTC ACTGCCAGTA AAGTCCAAGT ATCACTCTAT GGGAGTCTCT GGGATTGAA CAAATCTGC TACAAGTCAG  
CGTGAACCG AGGTGGAGGT CCGTCGGGAG TGACGGTTCAT TTCAGGTTCA TAGTGAGATA CCTTTCAGGA CCTTAACTT GTTTTAGAG ATGTTCAATC

201 GAGTTCCTCT TATTGAAAT GGAATGATTG AGCGGATGAT TGAGAAGCTG TTTCCGTGCG TGATCCTCAC CCCCCTCGAC TGCTTCTGG AGGAGGCCAA  
CTCAAGGGGA ATAACTTTTA CCTTACTAAC TCGCCTACTA ACTCTTCGAC AAAGGCACGC ACTAGGAGTG GGGGAGCTG AGGAAGACCC TCCCTCGGTT

301 ACTCCAAGG GGTCCGCCT ACCTGCCGCT CCCAATGAG CTCACGAGCT GAGTGGGGC TGCCATGCT TCTCCACAA ATTCAATGCAC TGGCAGGAGG  
TGAGGTTCCC CCGAGGCGA TGGACGGCGA GGGTTACACC GATGCTCTGA CTCACCCCG ACGGTACCGA AGAGGGTGT TAAGTACGTG ACCGTCTCTC

401 AATTGCTGCT GGGAGGCATG GCCAGAGACC CCCAAGGAGA GCTGTGAGG GCAGAGGCC TGCAGAGCAC CTTCTTGCTG ATGAGTCCCC GCCAGCTGTA  
TTAACGACGA CCTCCGTAC CCGTCTCTG GGGTTCCTCT CGACGACTCC CGTCTCCGG ACGTCTCGTG GAAGAAGCAC TACTCAGGG CCGTCGACAT

501 CGAGCATTC CGGGGTGACT ATCAGACACA TGACATTGGC TGGAGTGAGG AGCAGGCCAG CACAGTGCTA CAAGCCTGGC AGCGCGCTT TGTGCAGGTC  
GCTCGTAAAG GCCCCACTGA TAGTCTGTGT ACTGTAAACG ACCTCACTCC TCGTCCGGTC GTGTACGAT GTTCGGACCG TCGCCCGCAA ACAGTCCAG

601 GGTATGGACA AGGACAGGG GGTGCCCTGA GGCCATTCCC TCCTCCTGCC CCCTCCTATC CACCCTGTTT CTCCAGTGG CCCAGGAGGC CTGCTCTGAG  
CCATACCTGT TCCTGTCCCC CCACGGGACT CCGGTAAGG AGGAGGACCG GGGAGGATAG GTGGGACAA GAGGTGACG GGTCTCTCCG GACCGGACTC

701 AACGTTTCCC AGCAGATCCA TGCTTCTCC TCCACCACC TGGATGACAT CCTGCATCG TTCTCTGAAG TCAGTGTGTC CCGTGTGCTG GGAGGCTATC  
TTGCCAAGG TCGTCTAGGT ACGGAAGAGG AGGTGGTGG ACCTACTGTA GGACGTACCG AAGAGACTTC AGTCAGGAG GGCACACCAC CCTCCGATAG

801 TGCTATGGT GGTCTTGA CCTGGCACCT TGCCCCCACC CCACCTCCA CCAGTCCCCA CCTGGGGAG CCCCTGAGAC TGCCCTTTTC CCCCACAGCT  
ACGAGTACCA CCCAGAACGT GGACCGTGA ACGGGGTGG GTGGAGGTT GTTACCGGT GGGACCCCTC GGGGACTCTG ACGGGAAGG GGGGTGTCGA

FIG. 10A

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901 GGCCTATGCC TGTGTGACCA TGCTGCGGTG GGACTGCCCG CAGTCCGAGG GTTCCGTGGG CTTTGCCGGG GTACTGCTGG TGSCCCTGGC GGTGGCCTCA  
CCGGATACGG ACACACTGGT ACGACGCCAC CCTGACGCGG GTCAGGCTCC CAAGGCACCC GGAACGGCCC CATGACGACC ACCGGGACCG CCACCGGAGT  
1001 GGCCTTGGGC TCTGTGCCCT GCTCGGCATC ACCTTCAATG CTGCCACTAC CCAGGTACGC CAGGACTGCA GGGCAGACTC AGTGCCAGTC ACCAGGCTTC  
CCGGAACCCG AGACACGGGA CGAGCCGTAG TGAAGTTAC GACGGTGATG GGTCATGCG GTCCTGACGT CCCGTCTGAG TCACGGTCAG TGGTCCGAAG  
1101 ACGGCTCTC AGCTGCCCGC TCCTCTGCC CTCCAGGTGC TGCCCTTCTT GACTCTGGGA ATCGGCGTGG ATGACGTATT CCTGTGGCG CATGCCCTCA  
TGCCCAGGAG TCGACGGCG AGGACGGG GAGGTCCACG ACGGAAGAA CTGACACCT TAGCCGCACC TACTGCATAA GGACGACCGC GTACGGAGT  
1201 CAGAGGCTCT GCCTGGCACC CCTCTCCAG TGGGGCCTTG TCCCCACGGG CTCACTGAG GCAGCTCAGC TTACTGGTTA AGAGCTCTT GGTCAAGTG  
GTCTCCGAGA CCGACCGTGG GGAGAGTCC ACCCCGGAAC AGGGGTCCC GAGTAGACTC CGTCAGTGG AATGACCAAT TCTCGAGAA CCAAGTTCC  
1301 ACCTTGGGCT GCTAATGAAC CTCGGTGCCT CTTGTCCCA TGTGTAAACA GGGGAAATAA TAGTGCTGG TCCTAAGGGT TATTGTTGG ATCAGTGAAG  
TGGAACCCGA CGATTACTTG GAGCCACGGA GAACAGGGGT ACACATTGT CCCCTTATT ATCACGACAC AGGATTCCCA ATAACAACC TAGTCACTTC  
1401 TAACTCAAGT TGAATGTTA GAACAGCCCA TCATACGTAC ATGGTACCCA ATAAATGCTA GCCACTGTGT TATGACTGCC CCACCTCTGC ACCCAAGTT  
ATTGAGTTCA ACTTACGAAT CTTGTGCGGT AGTAGCATG TACCATGGGT TATTACCAT CGGTGACACA ATACTGACGG GGTGGAGACG TGGGTTCAA  
1501 CCTGAGCCTC CCCTTCACTC CACTTTGACA CGGCCCTCC CTTGTGACCT GAGGGCAGGT CCCCACTCTG TCCTGGCAGG AGCGCATGG CGAGTGTCTG  
GGACTCGGAG GGAAGTGAG GTGAATGT GCGCGGAGG GAACACTGGA CTCCGTCCA GGGGTGAGAC AGGACCTGC TCGCGTACCC GCTCACAGAC  
1601 CAGCGCACGG GCACCAGTGT TGTACTCACA TCCATCAACA ACATGGCCGC CTTCTCATG GCTGCCCTCG TTCCCATCCC TCGGCTGCGA GCCTTCTCCC  
GTCCGCTGCC CGTGGTCACA ACATGAGTGT AGGTAGTGT TGTACCGGCG GAAGGAGTAC CGACGGGAGC AAGGGTAGGG ACGCGACGCT CGGAAGAGGG  
1701 TACAGCCTGG ACCTACGGG CGGCCACTGC CAGCGCCTTG ATGTGCTCTG CTGCTTCTCC AGGTACTGCC TGCGCCCCAG CCCCTTCTC CCGTGACCCA  
ATGTCGGACC TGGATGCCGC CGCGGTGACG GTCGCGGAAC TACACGAGAC GACGAAGAGG TCCATGACGG ACGCGGGTGC GGGGAAGGAG GGCACCTGGT  
1801 CGCCAGCCTG TCCCTCACC AGCATTTCAA AGCATTTCAA GGCACAGACC TGTCTATCC TCTCTACCTC TTCCAGTCCC TGCTCTGCTC AGGTGATTCA GATCCTGCC  
GCGTGGGAC AGGGGAGTGG TCGTAAAGTT CCGTGTCTGG ACAGTAGGTG AGAGATGGAG AAGGTACGGG ACGAGACGAG TCCACTAAGT CTAGGACGGG  
1901 CAGGAGCTGG GAGACGGGAC AGTACCAGTG GGCATTGCC ACCTACTGC CACAGTTCAA GCCTTTACCC ACTGTGAGC CAGCAGCCAG CATGTGGTCA  
GTCTCGACC CCCTGCCCTG TCATGGTCA CCGTAACGGG TGGAGTGACG GTGTCAAGT CCGAAATGGG TGACACTTCG GTCGTGGTGC GTACACCAGT  
2001 CCATCTCTGCC TCCCAAGCC CACCTGGTGC CCCCACCTTC TGACCCACTG GGCTCTGAGC TCTTCAGCCC TGGAGGTCC ACACGGGACC TTCTAGGCCA  
GGTAGGACGG AGGGTTCCG GTGGACCACG GGGGTGGAAG ACTGGGTGAC CCGAGACTCG AGAAGTCCGG ACCTCCAGG TGTGCCCTGG AAGATCCGGT

FIG. 10B

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2101 GGAGGAGGAG ACAAGGCAGA AGGCAGCCTG CAAGTCCCTG CCTGTGCCC GCTGGAATCT TGCCCATTTT GCCCGCTATC AGTTTGCCCC GTTGCTGCTC  
CCTCCTCCTC TGTTCCTCT TCCGTCCGAC GTTCAGGGAC GGGACACGGG CGACCTTAGA ACGGGTAAAG CCGGGCGATAG TCAAACGGGG CAACGACGAG

2201 CAGTCACATG CCAAGGCCAT CGTCTGGTG CTCTTTGGTG CTCTTCTGGG CCTGAGCCTC TACGGAGCCA CCTTGGTGCA AGACGGCCTG GCCCTGACGG  
GTCAGTGATC GGTTCGGTA GCACGACCAC GAGAAACCAC GAGAAGACCC GGAATCGGAG ATGCCTCGGT GGAACCACTT TCTGCCGGAC CGGACTGCC

2301 ATGTGGTCC TCGGGGCACC AAGGAGCATG CCTTCCTGAG CGCCAGCTC AGTACTTCT CCCTGTACGA GGTGGCCCTG GTGACCCAGG GTGGCTTTGA  
TACACCACGG AGCCCGGTGG TTCTCTGTAC GGAAGGACTC GCGGGTCGAG TCCATGAAGA GGGACATGCT CCACCGGAC CACTGGGTCC CACCGAAACT

2401 CTACGCCCAC TCCCAACGGG CCTCTTTGA TCTGCACCAG CGCTTCAGTT CCTCAAGGC GTGTCTGCC CCACCGGCCA CCCAGGCACC CCGACCTGG  
GATCGGGTG AGGTTGGC GGGAGAACT AGACGTGGTC GCGAAGTCAA GGGAGTTCCG CCACGACGGG GGTGGCCGGT GGTCCGTGG GCGTGGAC

2501 CTGCACTATT ACCGCAACTG GCTACAGGGA ATCCAGGCTG CCTTTGACCA GGAATGGGT TCTGGGGCA TCACCCGCCA CTCGTACCGC AATGGCTCTG  
GACGTGATAA TGGCGTTGAC CGATGTCCT TAGGTCCGAC GGAATGGT CCTGACCCGA AGACCCGGT AGTGGCGGT GAGCATGGG TTACCGAGAC

2601 AGGATGGGG CCTGGCCTAC AAGCTGCTCA TCCAGACTGG AGACGCCAG GAGCCTCTGG ATTTACAGCCA GGTGGGAGA GGGCTGGAG GGTCCACTAG  
TCTTACCCG GGACCGGATG TTCGACGAGT AGGTCTGACC TCTCGGGTC CTCGGAGACC TAAAGTCGGT CCAACCTCT CCCGACCTCC CCAGTGTATC

2701 TACAGGGGT GCAGGCCTCC TGGGCCCAGG CCTTCAGCCC TCTCTGCCCTC TGCAGTGCAC CACAAGGAAG CTGGTGGACA GAGAGGACT GATTCCACCC  
ATGTCCCCGA GTCCGGAG ACCCGGTCC GGAAGTCGGG AGACACGGAG ACGTCTGCTC GTGTTCTTTC GACCACCTGT CTCTCCCTGA CTAAGGTGGG

2801 GAGTCTTCT ACATGGGGCT GACCGTGTGG GTGAGCACTG ACCCCCTGGG TCTGGCAGCC TCACAGGCCA ACTTCTACCC CCCACCTCTT GAATGGCTGC  
CTCGAGAAGA TGTACCCCGA CTGGCACACC CACTCTCTAC TGGGGACCC AGACCGTCCG AGTGTCCGGT TGAAGATGGG GGGTGGAGGA CTTACCGAGC

2901 ACGACAAATA CGACACCACG GGGGAGAAC TTGCGCAGTGA GTCTTGGGG GAGCTCGGCA AGAGCCTCAG CCTCGCCAC ACAAGCCCTG AGCCTGAGGC  
TGCTGTTTAT GCTGTGGTGC CCCCTCTTGG AAGCGTCACT CAGAACCCCT CTCGAGCCCT TCTCGAGTC GGAGGGGTG TGTTCGGAC TCGGACTCCG

3001 CCTGCCCACT CTGCCCGGTG CTCACCGCCC TGTCCCTCTC CCTCTTCTCC CTTCCTCAGT CCGGCAGCT CAGCCCTGG AGTTTGCCCA  
GGACGGGTGA GACGGGGCAC GAGTGGCGG ACAGGGAGAG GGAGAGAGG GAAGGGGAGG GGAGGTCTCA GGGCGGTCTGA GTCGGGAACC TCAAACGGGT

FIG. 10C

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3101 GTTCCCTTC CTGCTGCGTG GCCTCCAGAA GACTGCAGAC TTTGTGGAGG CCATCGAGGG GGCCCGGGCA GCATGCGCAG AGCCCGGCCA GGCTGGGGTG  
CAAGGGGAAG GACGACGCAC CGGAGGTCTT CTGACGTCTG AACACCTCC GGTAGTCCC CCGGGCCCGT CGTACGCGTC TCCGGCCGGT CCGACCCAC  
3201 CACGCCCTACC CCAGCGGCTC CCCCTTCCTC TTCTGGGAAC AGTATCTGGG CCTGCGCGCG TGCTTCCTGC TGGCCGTCTG CATCTGCTG GTGTGCACTT  
GTGCGGATGG GGTGCGCGAG GGGGAAGGAG AAGACCCTTG TCATAGACCC GGACGCGCGG ACAGAGGACG ACCGGCAGAC GTAGGACGAC CACACGTGAA  
3301 TCCTCGTCTG TGCTCTGCTG CTCCTCAACC CCTGGACGGC TGCCCTCATA GTGAGTGCTT GCAGGAGTGG GGACAGAGAC ACCCCACCTT TCCCTGCCCA  
AGGAGCAGAC ACAGACGCAC GAGGAGTTGG GGACTGCGG ACCGGAGTAT CACTACGAA CGTCTCACC CTTGTCTCTG TGGGGTGGGA AGGACCGGT  
3401 GCCTGTCTC CCTCCTGCCA GGAGCCCTCT GTGAGCCCTG TCTCCCTCAG GTGCTGGTCC TGGCGATGAT GACAGTGGAA CTCTTTGTA TCATGGGTTT  
CGACAGTAG GGAGGACGGT CCTCGGAGA CACTCGGGAC AGAGGGAGTC CAGGACCAGG ACCGTACTA CTGTCACTT GAGAAACCAT AGTACCCAAA  
3501 CTGGGGCATC AAGCTGAGTG CCATCCCGGT GGTGATCCTT GTGSCCTCTG TAGGCATTGG CGTTGAGTTC ACAGTCCACG TGGCTCTGTT GAGCACGGGC  
GGACCCGTAG TTCGACTCAC GGTAGGGCA CCACTAGGAA CACCGGAGAC ATCCGTAACC GCAACTCAAG TGTCAGGTGC ACCGAGACCA CTCGTGCCCG  
3601 ACCCGGGGA GGGACCAATC AGCTGATTCA GTATTCAACA CATATTGTTT AAGCCCTAC TATGTGCTAG GTACTATTTA AGAATTGGG CTGGGTGGAC  
TGGGSCCCT CCTGGTTAG TCGACTAAGT CATAAGTTGT GTATAACAAG TTCGGGGATG ATACACGATC CATGATAAAT TCTTAAACCC GACCCACCTG  
3701 GTGGTGGCTC ATTCTGTAA TCCCAGCACT TTGGGAGGCC GAGGCGGGTG GATCACCTGA GGTCGGGAGT TCGAAACCAG CCTGGCCAAC ATGGTGAAAC  
CACCAACCGAG TAAGGACATT AGGTCTGTGA AACCTCCGG CTCGCCCCAC CTAGTGGACT CCAGCCCTCA AGCTTGGTC GGACCGGTTG TACCACCTTG  
3801 CCTGTCTTTA CTAAAAATAC AAAAAATTAG CCAGGCGTGG TGGACATGC CAGTAGTCCC AGCTACTTTG GAGGTGAGG CAGAATTGCT TGAACCTGGG  
GGACAGAAAT GATTTTATG TTTTITATC GGTCCGCACC ACCGTGTACG GTCATCAGGG TCGATGAAAC CTCGACTCC GTCTTAACGA ACTTGGACCC  
3901 AGGCGAAGGT TGCAGTGAGC TGAGATCGTG CCATTGCACT CCAGCCTGGG CAACAAGAGT GCAACTCTCC GTCTCAAAA AAAAAAAA AAGGGCGGCC  
TCCGCTTCCA ACCTCACTCG ACTCTAGCAC GGTACGTTGA GGTGCGACCC GTTGTCTCA GGTGAGAGG CAGAGTTTTT TTTTTTTTTT TTCCCGCCGG

4001 GCGA  
CGCT

FIG. 10D

~~clone 16-1 - human patched 2~~  
~~length - 2002 bp~~

(SEQ ID NO: 9)

1 TTCCGGCATG ACTCGATCGC GCGCCCTCAG AGAGCTGCC CCGAGTTACA CACCCCCAGC TCGAACCGCA GCACCCAGG TCCTAGCTGG GAGCCTGAAG  
AAGCCGTAC TGAGCTAGG GCGGGAGTC TCTCGACGG GGTCAATGT GTGGGGTGC AGCTTGGCGT CGTGGGTCT AGGATCGACC CTCGACTTC

101 GCTCCACTCT GGTTCGTGC TTACTTCCAG GGCCTGCTCT TCTCTCTGG ATCGGGGATC CAGAGACATT GTGGCAAGT GCTCTTCTG GACTGTGTTGG  
CGAGGTGAGA CCGAAGCAG AATGAAGTC CCGGACGAGA AGAGAGACC TACGCCCTAG GTCTCTGTAA CACCGTTTCA CGAGAAAGAC CCTGACAACC

201 CCTTTGGGCG CTGGGCATTA GGTCTCCGCA TGGCCATTAT TGAGACAAAC TTGGAAACAG TCTGGGTAGA AGTGGGCAGC CGGGTGAGCC AGGAGCTGCA  
GGAAACCCCG GGACCGTAAT CCAGAGCGGT ACCGGTAATA ACTCTGTTG AACCTGTG AGACCCATCT TCACCCGTCG GCCCACTCGG TCCTCGACGT

301 TTACACCAAG GAGAAGCTGG GGGAGGAGGC TGCATACACC TCTCAGATGC TGATACAGAC CGCACGCCAG GAGGGAGAGA ACATCCTCAC ACCCGAAGCA  
AATGTGGTTC CTCCTCGACC CCTCCTCCG ACGTATGTGG AGAGTCTACG ACTATGCTG GCGTGGGTC CTCCTCTCT TGTAGGAGTG TGGGCTTCGT

401 CTTGGGCTCC ACCTCCAGGC AGCCCTCACT GCCAGTAAAG TCCAAATATC ACTCTATGG AGTCTCTGG ATTTGAACAA AATCTGCTAC AAGTCAGGAG  
GAACCGGAG TGGAGGTCCG TCGGGAGTGA CCGTCAATTC AGGTTTATAG TGAGATACCC TTCAGGACCC TAAACTTGT TTAGACGATG TTCAGTCTCTC

501 TTCCCTTAT TGAAAATGGA ATGATTGAGT GGATGATTGA GAAGCTGTTT CCGTGGGTGA TCCTCACCCC CCTCGACTGC TTCTGGGAGG GAGCCAAACT  
AAGGGGATA ACTTTTACCT TACTAACTCA CCTACTAACT CTTCGACAAA GGCACGCACT AGGAGTGGGG GGAGCTGACG AAGACCTCC CTCGGTTTGA

601 CCAAGGGGCG TCCGCTTACC TGCCCGGCGG CCGGATATC CAGTGGACCA ACCTGGATCC AGACAGCTG CTGGAGGAGC TGGGTCCCTT TGCCTCCCTT  
GGTTCCCGCG AGCGGATGG ACGGCGCGG GGGCCTATAG GTCACCTGGT TGGACCTAGG TCTCGTCGAC GACCTCCTCG ACCCAGGGA ACGGAGGGA

701 GAGGGCTTCC GGGAGCTGCT AGACAAGGCA CAGGTGGGCG AGGCTACGT GGGCGGCGCC TGCTGTCACC CTGATGACCT CCACTGCCCA CCTAGTGCCC  
CTCCCGAAG CCCTCGACGA TGTGTTCCGT GTCCACCCG TCCGGATGCA CCGCGCGGG ACAGACGTGG GACTACTGGA GGTGACGGGT GGATCAGCGG

801 CCAACCATCA CAGCAGGCGC GTTCCCAATG TGGCTCACGA GCTGAGTGG GGCTGCCATG GCTTCTCCCA CAAATTCATG CACTGGCAGG AGGAATTGCT  
GGTTGGTAGT GTCGTCCGTC CGAGGGTTAC ACCAGTGCT CCACTACCC CCGACCGTAC CGAAGAGGGT GTTTAAGTAC GTGACCGTCC TCCTTAACGA

901 GCTGGGAGGC ATGGCCAGAG ACCCCCAAGG AGAGCTGCTG AGGGCAGAG CCCTGACAG CACTTCTTG CTGATGAGTC CCCGCCAGCT GTACGAGCAT  
CGACCCCTCG TACCGGTCTC TGGGGTTCC TCTCGACGAC TCCGCTCTCC GGGACGTCTC GTGGAAGAAC GACTACTCAG GGGCGGTGCA CATGCTCGTA

FIG. 11A

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1001 TTCCGGGGTG ACTATACAGAC ACATGACATT GGCTGGAGTG AGAGCAGGC CAGCACAGTG CTACAAGCCT GGCAGCGGCG CTTTGTGCAG CTGGCCCCAGG  
AAGGCCCCAC TGATAGTGTG TGTAAGTGTAA CCGACCTCAC TCCTCGTCCG CTCGTGTAC GATGTTCCGA CCGTCGCCGC GAAACACGTC GACCGGGTCC

1101 AGGCCCTGCC TGAGAACGCT TCCCAGCAGA TCCATGCCCT CTCCTCCACC ACCCTGGATA ACATCCTGCA TCGGTTCTCT GAATCAGTG CTGCCCGTGT  
TCCGGGACGG ACTCTTGCGA AGGTCTGTCT AGGTACGGAA GAGGAGGTGG TGGGACCTAT TGTAGACGT ACGCAAGAGA CTTAGTCAC GACGGGCACA

1201 GGTGGGAGGC TATCTGTCTA TGCTGSCCTA TGCTGTGTG ACCATGCTGC GGTGGACTG CGCCAGTCQ CAGGTTCCG TGGCCTTG CCGGGTACTG  
CCACCTCCG ATAGACGAGT ACGACCGAT ACGGACACAC TGGTACGACG CCACCTGAC GCGGTTCAGG GTCCCAAGGC ACCCGAAGC GCCCATGAC

1301 CTGGTGGCCC TGGCGGTGGC CTCAGGCCCT GGGCTCTGTG CCTGTCTGG CATCACCTTC AATGCTGCCA CTACCCAGGT GCTGCCCTTC TTGGCTCTGG  
GACCACCGG ACCGCCACCG GAGTCCGGAA CCGGAGACAC GGGACGAGCC GTAGTGGAG TTACGACGT GATGGGTCCA CGACGGGAG AACCGAGACC

1401 GAATCGGCGT GGATGACGTA TTCTGTGTG CGCATGCCCT CACAGAGGT CTGCCCTGGA CCCCTCTCCA GGAGCGCATG GCGAGTGTG TGCAGCGCAC  
CTTAGCCGCA CCTACTGCAT AAGGACGACC CGTCTCCGA GCGGACCGT GGGGAGAGGT CCTCGCGTAC CCGCTCACAG ACGTCGCGTG

1501 GGGACACCAGT GTCGTACTCA CATCCATCAA CAACATGGCC GCCTCTCTCA TGGCTGCCCT CGTTCCTATC CTTGCCCTCTC CTTACAGCCA  
CCCGTGGTCA CAGCATGAGT GTAGGTAGTT GTTGTACCG CGGAAGGAGT ACCGACGGGA GCAAGGTAG GGACCGGACG CTCGGAAGAG GAATGTCGTT

1601 TCCTCAGCCT GGACCTACGG CCGCGCCACT GCCAGCGCT TGATGTCTC TGCTGCTTCT CCAGTCCCTG CTCTGCTCAG GTGATTCAGA TCCTGCCCCA  
AGGAGTCGGA CCTGGATGCC GCGCGGTGA CGGTCCGGA ACTACAGAG ACGACGAAGA GGTACGGAC GAGACGAGTC CACTAAGTCT AGGACGGGGT

1701 GGAGCTGGG GACGGGACAG TACCAGTGGG CATTGCCAC CTCATGCCA CAGTTCAAGC CTTTACCCAC TGTGAAGCCA GCAGCCAGCA TGTGTCACC  
CCTCGACCCC CTGCCCTGTC ATGCTCACC GTACCGGTG GAGTACCGT GTCAAGTTG GAAATGGTG AACCTTCGT CGTGCGTCTG ACACCAAGTG

1801 ATCCTGCCCT CCAAGCCCA CCTGGTGCC CCACCTCTG ACCCACTGGG CTCGAGCTC TTCAGCCCTG GAGGTCAC ACGGACCTT CTAGGCCAGG  
TAGGACGGAG GGGTTCGGT GGACCACGG GGTGGAGAC TGGGTGACCC GAGACTCGAG AAGTCGGAC CTCCAGGTG TGCCCTGGAA GATCCGGTCC

1901 AGGAGGAGAC AAGCAGAAAG GCAGCCTGCA AGTCCCTGCC CTGTGCCCGC TGGAACTCTG CCCATTTCGC CCGGAATTC CTGCAGCCCG GGGGATCCAC  
TCCTCTCTG TTCCGCTTC CGTCGACGT TCAGGACGG GACACGGCG ACCTAGAAC GGGTAAAGCG GGGCCTTAAG GACGTCGGG CCCCTAGGTG

2001 TAGTCTAGA GCGGCCGCCA CCGCGGTGA GCTCCAGCTT TTGTTCCCTT TAGTGAGGT TAATTGCGG CTTGGGTATC TT  
ATCAGATCT CGCCGGCGT GCGGCCACCT CGAGTCTGAA AACAAAGGAA ATCACTCCCA ATTAACGCG GAACCATAG AA

FIG. 11B

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